

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 08:48:08 ; Search time 34.7668 Seconds  
(without alignments)  
913.271 Million cell updates/sec

Title: US-10-000-439-2

Perfect score: 1764

Sequence: 1 ASTKCPVFPFLAPSSKSTSG.....MHEALHNHYQKSLSPGK 330

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1729	98.0	330	1 GHHU	Ig gamma-1 chain C
2	1592.5	90.3	377	2 A23511	Ig gamma-3 chain C
3	1590.5	90.2	377	2 A60764	Ig gamma-3 chain C
4	1566	88.8	326	1 G4HU	Ig gamma-2 chain C
5	1552.5	88.0	327	1 G4HU	Ig gamma-4 chain C
6	1225.5	69.5	374	2 S69339	Ig heavy chain V r
7	1225	69.4	328	2 I47159	Ig gamma 2a chain
8	1222	69.3	255	4 S31866	Ig gamma-1 chain C
9	1219	69.1	328	2 I47160	Ig gamma 2b chain
10	1216	68.9	234	2 PT0207	Ig gamma chain C r
11	1193	67.6	328	2 I47158	Ig gamma 1 chain c
12	1192.5	67.6	323	1 GHRB	Ig gamma chain C r
13	1189	67.4	328	2 I47161	Ig gamma 3 chain c
14	1174.5	66.6	329	1 G2GP	Ig gamma-2 chain C
15	1163.5	66.0	472	2 S31459	Ig gamma-1 chain -
16	1144.5	64.9	470	2 S22080	Ig heavy chain pre
17	1125.5	63.8	308	2 C30554	Ig heavy chain C r
18	1123	63.7	289	1 G3HUM1	Ig gamma-3 heavy c
19	1117.5	63.4	333	2 PS0018	Ig gamma-2b chain
20	1116	63.3	444	2 PC4436	monoclonal antibody
21	1114	63.2	326	2 PS0017	Ig gamma-1 chain C
22	1109	62.9	324	1 G1MS	Ig gamma-1 chain C
23	1108	62.8	329	1 G3MSC	Ig gamma-3 chain C
24	1104	62.6	393	1 G3MSC	Ig gamma-1 chain C
25	1097	62.2	398	1 G3MSC	Ig gamma-3 chain C
26	1093	62.0	330	1 G2MSA	Ig gamma-2a chain
27	1093	62.0	469	2 S37483	Ig gamma-2a chain
28	1090.5	61.8	335	1 G2MSAB	Ig gamma-2a chain
29	1088	61.7	399	1 G2MSAM	Ig gamma-2a chain

30	1085.5	61.5	329	2 S00847	Ig gamma-2c chain
31	1078	61.1	446	2 S40295	Ig gamma-2a chain
32	1074	60.9	322	2 PS0019	Ig gamma-2a chain
33	1063.5	60.3	327	2 S06611	Ig gamma-2 chain C
34	1054	59.8	405	1 G2MSBM	Ig gamma-2b chain
35	1039	58.9	475	2 S01321	Ig gamma-2b chain
36	1036.5	58.8	474	1 G2MS11	Ig gamma-2b chain
37	1028	58.3	277	2 I47162	Ig gamma 4 chain c
38	669	37.9	180	2 I46732	Ig epsilon heavy cha
39	648.5	36.8	548	2 S38864	Ig epsilon chain C
40	549	31.1	249	2 S69340	Ig heavy chain VH1
41	547	31.0	218	2 A36040	Ig heavy chain V-I
42	547	31.0	549	2 S04845	Ig heavy chain pre
43	542	30.7	152	2 S14236	Ig gamma-1 chain C
44	534	30.3	220	2 A49444	Ig gamma-1 heavy c
45	532	30.2	241	2 S69131	Ig heavy chain (DO

#### ALIGNMENTS

##### RESULT 1

GHHU  
Ig gamma-1 chain C region - human

C/Species: Homo sapiens (man)

C/Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #ext change 09-Jul-2004

C/Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146

R/Elison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A/Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A/Reference number: A93433; M0ID:82274238; PMID:6287432

A/Accession: A93433

A/Molecule type: DNA

A/Residues: 1-330 <BL>

A/Cross-references: UNIPROT:P01957; EMBL:Z17370

A/Note: This sequence has the Gln(17) allotypic marker, 97-Lys, and the Gln(1) markers, 2

A/Note: Lys-330 is removed after translation

R/Harris, L.J.

submitted to the EMBL Data Library, October 1992

A/Reference number: S33904

A/Accession: S36861

A/Molecule type: DNA

A/Residues: 2-330 <HAR>

A/Cross-references: EMBL:Z17370

R/Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A/Title: Structure of human immunoglobulin gamma genes: implications for evolution of a

A/Reference number: S33887; M0ID:83001943; PMID:6811139

A/Accession: S33887

A/Molecule type: DNA

A/Residues: 88-113;235-330 <TAK>

A/Cross-references: EMBL:Z17370

R/Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C

Biochemistry 9, 3161-3170, 1970

A/Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequenc

A/Reference number: A90563; M0ID:71064024; PMID:5489771

A/Contents: myeloma protein Bu

A/Accession: B90563

A/Molecule type: protein

A/Residues: 1-96; 'R', 98-135 <GUN>

A/Note: this sequence has the Gln(3) marker, 97-Arg

R/Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A/Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequer

A/Reference number: A90564; M0ID:71064025; PMID:5530842

A/Contents: Bu

A/Accession: A90564

A/Molecule type: protein

A/Residues: 136-154; 'Q', 156-165; 'Q', 167-176; 'Q', 178-197; 'D', 199-238; 'E', 240; 'H

Hope-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A/Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),



F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 90.2%; Score 1590.5; DB 2; Length 377;

Best Local Similarity 80.1%; Pred. No. 1.1e-102;

Matches 302; Conservative 13; Mismatches 15; Indels 47; Gaps 1;

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QY 1 ASTKPSVFPPLAPSSKSTSGTALGCLVKDYFPEPVYTVSNMGSALTSGVHPFPAVLQSS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 ASTKPSVFPPLAPSSKSTSGTALGCLVKDYFPEPVYTVSNMGSALTSGVHPFPAVLQSS 60
    61 GLYSLSVTVTVSSSSLGITQTYICNVNHNKPSNTKVDKVV----- 98
    61 GLYSLSVTVTVSSSSLGITQTYICNVNHNKPSNTKVDKVELKTPPLGDTTTCRCRCPKSC 120
QY 99 -----EPKSCDKHTHTCPCPAPPELLGSPVFLFPPPKXDT 133
    121 DTPPCRCRCPKSCDTPPRCRCPKSCDTPPRCRCPAPPELLGSPVFLFPPPKXDT 180
Db 121 DTPPCRCRCPKSCDTPPRCRCPKSCDTPPRCRCPAPPELLGSPVFLFPPPKXDT 180
QY 134 LMISRTPEVTCVVDVSHEDPEVKFMVYDGYEVNHNKTKPREEQYNSTFRVSVLTVLH 193
    181 LMISRTPEVTCVVDVSHEDPEVKFMVYDGYEVNHNKTKPREEQYNSTFRVSVLTVLH 240
QY 194 QNMNNGKEVCKVSNKALPAPLEKITSKAKVQPREQVYTLPPSPDELTKNOVSLTCLVK 253
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 QNMNNGKEVCKVSNKALPAPLEKITSKAKVQPREQVYTLPPSPDELTKNOVSLTCLVK 300
QY 254 GFPPSDIAVEMESNGCPENNYKTPPEVLDSVGSFFLYSKLTVDKSRWQGNVFSQSVME 313
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 GFPPSDIAVEMESNGCPENNYKTPPEVLDSVGSFFLYSKLTVDKSRWQGNVFSQSVME 360
QY 314 ALHNHYQQRSLSLSPCK 330
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 ALHNHYQQRSLSLSPCK 377
```

#### RESULT 4

G2HU

Ig gamma-2 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text\_change 09-Jul-2004

C:Accession: A93906; A92809; A90752; A93133; A02148

R:Ellison, J.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982

A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con

A:Reference number: A93906; PMID:82197621; PMID:6804948

A:Accession: A93906

A:Molecule type: DNA

A:Residues: 1-326 <ELL>

A:Cross-References: UNIPROT: P01859; GB: V00554; GB: J00230; NID: G32759; PIDN: CAB58438.1; F

A:Note: Lys-326 is probably removed posttranslationally

R:Wang, A.C.; Tuny, E.; Pudenberg, H.H.

J. Immunol. 125, 1048-1054, 1980

A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and E

A:Reference number: A92809; PMID:81007873; PMID:6774012

A:Accession: A92809

A:Molecule type: protein

A:Residues: 119, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>

A:Note: Trp-156 is at or near the complement-binding site

R:Connell, G.E.; Parr, D.M.; Hofmann, T.

Can. J. Biochem. 57, 758-767, 1979

A:Title: The amino acid sequences of the three heavy chain constant region domains of a

A:Reference number: A90752; PMID:80001357; PMID:113060

A:Contents: myeloma protein Zie

A:Accession: A90752

A:Molecule type: protein

A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-

A:Note: this sequence has since been revised

R:Hofmann, T.; Parr, D.M.

Mol. Immunol. 16, 923-925, 1979

A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g

A:Reference number: A93133; PMID:80114419; PMID:118920

A:Contents: Zie

A:Accession: A93132

A:Molecule type: protein

A:Residues: 238-275 <HOF>

R:Hofmann, T.; Parr, D.M.

submitted to the Atlas, March 1980

A:Reference number: A94591

A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic

ned

R:Milstein, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.

A:Reference number: A90253; PMID:72033500; PMID:4940472

A:Contents: annotation; myeloma protein Sa, disulfide bonds

R:Frangione, B.; Milstein, C.; Pink, J.R.L.

Nature 221, 145-148, 1969

A:Title: Structural studies of immunoglobulin G.

A:Reference number: A93157; PMID:69064124; PMID:5782707

A:Contents: annotation; Sa, disulfide bonds

C:Genetics:

A:Gene: GDB:IGHG2

A:Cross-References: GDB:119338; OMIM:147110

A:Map position: 14q32.33-14q32.33

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a;

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>

F:133-202/Domain: immunoglobulin homology <IM2>

F:239-306/Domain: immunoglobulin homology <IM3>

F:14/Disulfide bonds: interchain (to light chain) #status experimental

F:27-83,140-200,246-304/Disulfide bonds: #status experimental

F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:176/Binding site: carbohydrate (Aa) (covalent) #status predicted

Query Match 88.8%; Score 1566; DB 1; Length 326;

Best Local Similarity 89.1%; Pred. No. 4.4e-101;

Matches 294; Conservative 15; Mismatches 17; Indels 4; Gaps 2;

```
QY 1 ASTKPSVFPPLAPSSKSTSGTALGCLVKDYFPEPVYTVSNMGSALTSGVHPFPAVLQSS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 ASTKPSVFPPLAPSSKSTSGTALGCLVKDYFPEPVYTVSNMGSALTSGVHPFPAVLQSS 60
    61 GLYSLSVTVTVSSSSLGITQTYICNVNHNKPSNTKVDKVPKSCDKHTHTCPCPAPPELLG 120
QY 61 GLYSLSVTVTVSSSSLGITQTYICNVNHNKPSNTKVDKVPKSCDKHTHTCPCPAPPELLG 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GLYSLSVTVTVSSSSLGITQTYICNVNHNKPSNTKVDKVPKSCDKHTHTCPCPAPPELLG 116
    121 PSVFLFPPPKDITLMISRTPEVTCVVDVSHEDPEVKFMVYDGYEVNHNKTKPREEQYN 180
QY 121 PSVFLFPPPKDITLMISRTPEVTCVVDVSHEDPEVKFMVYDGYEVNHNKTKPREEQYN 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 117 PSVFLFPPPKDITLMISRTPEVTCVVDVSHEDPEVKFMVYDGYEVNHNKTKPREEQYN 176
    181 STYRVSVTVTVHOMMNCKEYCKVSNKALPAPLEKITSKAKVQPREQVYTLPPSRDE 240
QY 181 STYRVSVTVTVHOMMNCKEYCKVSNKALPAPLEKITSKAKVQPREQVYTLPPSRDE 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 177 STYRVSVTVTVHOMMNCKEYCKVSNKALPAPLEKITSKAKVQPREQVYTLPPSRDE 236
    241 LTKNOVSLTCLVKGFPSPDIAVEMESNGCPENNYKTPPEVLDSVGSFFLYSKLTVDKSRW 300
QY 241 LTKNOVSLTCLVKGFPSPDIAVEMESNGCPENNYKTPPEVLDSVGSFFLYSKLTVDKSRW 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 237 LTKNOVSLTCLVKGFPSPDIAVEMESNGCPENNYKTPPEVLDSVGSFFLYSKLTVDKSRW 296
    301 QQGNVFSQSVMEALHNHYQQRSLSLSPCK 330
QY 301 QQGNVFSQSVMEALHNHYQQRSLSLSPCK 330
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 297 QQGNVFSQSVMEALHNHYQQRSLSLSPCK 326
```

#### RESULT 5

G4HU

Ig gamma-4 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 02-Apr-1982 #sequence revision 02-Apr-1992 #text\_change 09-Jul-2004

C:Accession: A90933; A80249; A02150

R:Ellison, J.; Hood, L.

DNA 1, 11-18, 1981

A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A:Reference number: A90933; WUID:83157104; PMID:6299662  
A:Accession: A90933  
A:Molecule type: DNA  
A:Residues: 1-327 <EL>  
A:Cross-references: UNIPROT:P01861  
A:Note: the sequence was determined from the germline gene  
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Mistein, C.  
Biochem. J. 117, 33-47, 1970  
A:Title: Human immunoglobulin subclases. Partial amino acid sequence of the constant  
A:Reference number: A90249; WUID:70207560; PMID:4192699  
A:Accession: A90249  
A:Molecule type: protein  
A:Residues: 1-30;81-326 <PIN>  
C:Genetics:  
A:Gene: GDB:IGHG4  
A:Cross-references: GDB:119340; OMIM:147130  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1, 111/1, 221/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:99-110/Region: hinge  
F:134-203/Domain: immunoglobulin homology <IM2>  
F:240-307/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83,141-201,247-305/Disulfide bonds: #status predicted  
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:177/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 88.0%; Score 1552.5; DB 1; Length 327;  
Best Local Similarity 88.8%; Pred. No. 3.8e-100;  
Matches 293; Conservative 15; Mismatches 19; Indels 3; Gaps 1;

QY 1 ASTGSPVPLAPSSKSTSGTAAAGCLVKDYFPEPVYVSNNGALTSQHTFPAYLQSS 60  
DB 1 ASTGSPVPLAPSSKSTSGTAAAGCLVKDYFPEPVYVSNNGALTSQHTFPAYLQSS 60  
QY 61 GLYSLSVTVVSSSLGTYICNNVHKPSNTRKVDKVPKSCDKHTPCPPAPPELLGG 120  
DB 61 GLYSLSVTVVSSSLGTYICNNVHKPSNTRKVDKVPKSCDKHTPCPPAPPELLGG 117  
QY 121 PSVFLPPEPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180  
DB 121 PSVFLPPEPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 177  
QY 181 SYRYVSVLTIVHOMMNGEKYCKVKSNKALPAPKEKTSKAKVQPREPOVYTLPPSRDE 240  
DB 181 SYRYVSVLTIVHOMMNGEKYCKVKSNKALPAPKEKTSKAKVQPREPOVYTLPPSRDE 237  
QY 241 LTKNOVSLTCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDVSGVFLYSKLTVDKSRM 300  
DB 241 LTKNOVSLTCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDVSGVFLYSKLTVDKSRM 297  
QY 301 QGQNVFSCSVMEHALHNYQQRSLSPGK 330  
DB 301 QGQNVFSCSVMEHALHNYQQRSLSPGK 327

RESULT 6  
S69339  
Ig heavy chain V region precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #ext\_change 01-Dec-2000  
C:Accession: S69339; S72664  
R:Khamilichi, A.A.; Auncuturrier, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995  
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A:Reference number: S69339; WUID:95262687; PMID:7744049  
A:Accession: S69339  
A:Status: preliminary  
A:Molecule type: mRNA

A:Residues: 1-374 <KHA>  
A:Cross-references: EMBL:X81695  
R:Khamilichi, A.A.  
submitted to the EMBL Data Library, September 1994  
A:Reference number: S72664  
A:Accession: S72664  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140, C', 142-374 <KH2>  
A:Cross-references: EMBL:X81695  
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 69.5%; Score 1225.5; DB 2; Length 374;  
Best Local Similarity 87.1%; Pred. No. 1.8e-77;  
Matches 230; Conservative 6; Mismatches 17; Indels 11; Gaps 2;

QY 78 TQTYICNVN-----HK-PSNTKYDKKPEKSCDKHTPCPPAPPELLGSPVFLF 126  
DB 111 TATYICGVSVGGYGRFHSKGGTIVTVSSEPKSCDKHTPCPPAPPELLGSPVFLF 170  
QY 127 PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTRYV 186  
DB 127 PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTRYV 230  
QY 187 SVLTIVHOMMNGEKYCKVKSNKALPAPKEKTSKAKVQPREPOVYTLPPSRDELTKNOV 246  
DB 231 SVLTIVHOMMNGEKYCKVKSNKALPAPKEKTSKAKVQPREPOVYTLPPSRDELTKNOV 290  
QY 247 SLTCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDVSGVFLYSKLTVDKSRMQQGVNF 306  
DB 291 SLTCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDVSGVFLYSKLTVDKSRMQQGVNF 350  
QY 307 SCSVMHEALHNYQQRSLSPGK 330  
DB 351 SCSVMHEALHNYQQRSLSPGK 374

RESULT 7  
147159  
Ig gamma 2a chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #ext\_change 21-Jan-2000  
C:Accession: 147159  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s  
A:Reference number: 147159; WUID:95015845; PMID:7930579  
A:Accession: 147159  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: EMBL:U03779; NID:g433123; PID:AAA52217.1; PID:g433124  
C:Genetics:  
A:Gene: IGG2a  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IM4>

Query Match 69.4%; Score 1225; DB 2; Length 328;  
Best Local Similarity 67.5%; Pred. No. 1.7e-77;  
Matches 224; Conservative 46; Mismatches 56; Indels 6; Gaps 2;

QY 1 ASTGSPVPLAPSSKSTSGTAAAGCLVKDYFPEPVYVSNNGALTSQHTFPAYLQSS 60  
DB 1 AKPTAPSVPLAPCSRDTSGPNVALGLASSYFPEPVYVSNNGALTSQHTFPAYLQSS 60  
QY 61 GLYSLSVTVVSSSLGTYICNNVHKPSNTRKVDKVPKSCDKHTPCPPAPPELLGG 120  
DB 61 GLYSLSVTVVSSSLGTYICNNVHKPSNTRKVDKVPKSCDKHTPCPPAPPELLGG 116  
QY 121 PSVFLPPEPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180  
DB 121 PSVFLPPEPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 176



QY 181 STYRVSVTLVHONMNGEKCKVSNKALPAPIKTISSKAVQPREQVYTLPPSRDE 240  
Db 177 STYRVSVTLPIQHODMLNKEFKCKVNNKDLPAPIRIIISKAKGQTRPQVYTLPPHAE 236  
QY 241 LFNQVSLTCLVKGFPSPDIAYEWESNGO--PENNYKTTTPVLDVSGSFYLSKLTVDKS 298  
Db 237 LRSKVSITCLVIGFIPPIIDVEMQNGQPREBGNYRTTRTPQODVDGTFFLYSKFSVDKA 296  
QY 239 RMQGNVFSQSVMEALHNHYOQRSLSLSPGK 330  
Db 297 SWQGGGIFQCAVMEALHNHYQKSIKTPGK 328

## RESULT 8

S31866  
Ig gamma-1 chain C region - synthetic

C/Species: synthetic  
A/Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli  
C/Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000  
C/Accession: S31866  
R.Filipula, D.  
submitted to the EMBL Data Library, February 1993  
A/Description: Screening method for protein-protein interactions of cloned gene products.  
A/Reference number: S31866  
A/Accession: S31866  
A/Molecule type: mRNA  
A/Residues: 1-255 <FIL>  
A/Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49666.1; PID:g33069  
C/Keywords: immunoglobulin  
F.1-22/Region: Escherichia coli outer membrane protein A precursor  
F.23-255/Region: human Ig gamma-1 chain C region

Query Match 69.3%; Score 1222; DB 4; Length 255;  
Best Local Similarity 94.6%; Pred. No. 2e-77;

Matches 226; Conservative 3; Mismatches 10; Indels 0; Gaps 0;  
QY 92 TVDKKVEKSCDKTHTCPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSH 151  
Db 17 TVAQADVESKSCDKTHTCPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSH 76  
QY 152 EDPVKFNNYVDGVEVHNKTKPREQYNSTRYVSVTLVHONMNGEKCKVSNKAL 211  
Db 77 EDPVKFNNYVDGVEVHNKTKPREQYNSTRYVSVTLVHONMNGEKCKVSNKAL 136  
QY 212 PAPIKTISSKAVQPREQVYTLPPSRDELTKNQVSLTCLVKGFPSPDIAYEWESNGOPE 271  
Db 137 PAPIKTISSKAVQPREQVYTLPPSRDELTKNQVSLTCLVKGFPSPDIAYEWESNGOPE 196  
QY 272 NNYKTTTPVLDVSGSFYLSKLTVDKSRWQGNVFSQSVMEALHNHYOQRSLSLSPGK 330  
Db 197 NNYKTTTPVLDVSGSFYLSKLTVDKSRWQGNVFSQSVMEALHNHYOQRSLSLSPGK 255

## RESULT 9

I47160  
Ig gamma 2b chain constant region - pig (fragment)

C/Species: Sus scrofa domestica (domestic pig)  
C/Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C/Accession: I47160  
R.Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A/Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A/Reference number: I47158; MUID:95015845; PMID:7930579  
A/Accession: I47160  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-328 <KAC>  
A/Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126  
C/Genetics:  
A/Gene: IGG2b  
C/Superfamily: immunoglobulin C region; immunoglobulin homology  
F.113-202/Domain: immunoglobulin homology <IMM>

Query Match 69.1%; Score 1219; DB 2; Length 328;  
Best Local Similarity 67.2%; Pred. No. 4.3e-77;  
Matches 223; Conservative 45; Mismatches 58; Indels 6; Gaps 2;

QY 1 ASTKGSVPPLAPSSKSTSGTAAGCLVKDYFPEPVYTNMNGSLTSGVHPFPAVLAQS 60  
Db 1 APTKALVPLAPCGSDTGPVALAGCLAISSTYPPEVYTNMNGSLTSGVHPFPAVLAQS 60  
QY 61 GLYSLSVTVTPSSISGTQYICNVNHNKPSNTKVDKVRPKSCDKTHTCPCPAPPELLG 120  
Db 61 GLYSLSMTVTPASSLSKSTSYCNVNHPRATTKVDKRGVCTKTRPPDICAPESP----G 116  
QY 121 PSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYVDGVEVHNKTKPREQYN 180  
Db 117 PSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYVDGVEVHNKTKPREQYN 176  
QY 181 STYRVSVTLVHONMNGEKCKVSNKALPAPIKTISSKAVQPREQVYTLPPSRDE 240  
Db 177 STYRVSVTLPIQHODMLNKEFKCKVNNKDLPAPIRIIISKAKGQTRPQVYTLPPHAE 236  
QY 241 LFNQVSLTCLVKGFPSPDIAYEWESNGO--PENNYKTTTPVLDVSGSFYLSKLTVDKS 298  
Db 237 LRSKVSITCLVIGFIPPIIDVEMQNGQPREBGNYRTTRTPQODVDGTFFLYSKFSVDKA 296  
QY 239 RMQGNVFSQSVMEALHNHYOQRSLSLSPGK 330  
Db 297 SWQGGGIFQCAVMEALHNHYQKSIKTPGK 328

## RESULT 10

PT0207  
Ig gamma chain C region - chimpanzee

C/Species: Pan troglodytes (chimpanzee)  
C/Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 16-Jul-1999  
C/Accession: PT0207  
R.Shirlich, P.H.; Moustafa, Z.A.; Oestberg, L.  
Mol. Immunol. 28, 319-322, 1991  
A/Title: Nucleotide sequence of chimpanzee FC and hinge regions.  
A/Reference number: PT0207; MUID:91287716; PMID:2062315  
A/Accession: PT0207  
A/Molecule type: mRNA  
A/Residues: 1-234 <EHR>  
C/Superfamily: immunoglobulin C region; immunoglobulin homology  
C/Keywords: immunoglobulin  
F.48-117/Domain: immunoglobulin homology <IMM>

Query Match 68.9%; Score 1216; DB 2; Length 234;  
Best Local Similarity 95.7%; Pred. No. 4.6e-77;

Matches 224; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
QY 90 SNTKVDKVEKSCDKTHTCPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDV 149  
Db 1 SNTKVDKVEKSCDKTHTCPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDV 60  
QY 150 SHEDPEVKFNNYVDGVEVHNKTKPREQYNSTRYVSVTLVHONMNGEKCKVSNK 209  
Db 61 SHEDPEVKFNNYVDGVEVHNKTKPREQYNSTRYVSVTLVHONMNGEKCKVSNK 120  
QY 210 ALPAPIKTISSKAVQPREQVYTLPPSRDELTKNQVSLTCLVKGFPSPDIAYEWESNGO 269  
Db 121 ALPAPIKTISSKAVQPREQVYTLPPSRDELTKNQVSLTCLVKGFPSPDIAYEWESNGO 180  
QY 270 PENNYKTTTPVLDVSGSFYLSKLTVDKSRWQGNVFSQSVMEALHNHYOQRS 323  
Db 181 PENNYKTTTPVLDVSGSFYLSKLTVDKSRWQGNVFSQSVMEALHNHYOQRS 234

## RESULT 11

I47158

Ig gamma 1 chain constant region - pig (fragment)  
C/Species: Sus scrofa domestica (domestic pig)  
C/Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C/Accession: I47158

R.Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A>Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a B  
A:Reference number: 147158; MUID:95015845; PMID:7930579  
A:Accession: 147158  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: EMBL:U03778; NID:9433121; PIDN:AAA52216.1; PID:9433122  
A:Gene: IGG1  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IM3>  
  
Query Match 67.6%; Score 1193; DB 2; Length 328;  
Best Local Similarity 67.2%; Pred. No. 2.7e-75;  
Matches 223; Conservative 42; Mismatches 61; Indels 6; Gaps 3;  
  
Qy 1 ASTGSPVPLAPSSKSTGSGTAALGCLVKDYFPEPVYVSNNSGALTSQVHFPFPAVLQSS 60  
Db 1 AKTAPSVYPLAPCGRDVSGPVNALGCLASSYFPEPVYVSNNSGALTSQVHFPFPAVLQSS 60  
Qy 61 GLYSLSVVTVPSSSLGTQTYICNVNHRKSNTRKVDKVEPKSCDKHTHCPCPAPPELLGG 120  
Db 61 GLYSLSMTVTVASSLSKSTYCTCNVNHPTTKVDKRV--GIHQPTCTPCPGCE-VAG 116  
Qy 121 PSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVNNVTKRPREQYN 180  
Db 117 PSVFIFPPKPKDTLMISRTPEVTCVVDVSKHAIEVFGFQVYDGEVHNAETFRKPEQGN 176  
Qy 181 STYRVVSVLTVTHQWMMNKEKCKVSNKALPAPIEKITSKAKVQPREQVYVTLPPSRBE 240  
Db 177 STYRVVSVLTPIQHOMWLKGEKFKCKVNNVDLPAPITRTISKAIQGSREQVYVTLPPPAE 236  
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTPPVLDVSGSFYLLSKLTLDVS 298  
Db 237 LRSKVTLTCLVIGYIPPIIHVEWESNGQPEPEYTRITTPPODDVDGTRFPLSKLAVDKA 296  
Qy 299 RMQGNVFSGVMEALHNHYQOQSLSLSPGK 330  
Db 297 RWDGDKFECAVMEALHNHYQOQSLSLSPGK 328  
  
RESULT 12  
GHRB  
Ig gamma chain C region - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 24-Apr-1984 #sequence\_revision 15-Nov-1984 #text\_change 09-Jul-2004  
C:Accession: A91749; A90290; A93928; A90245; A94416; A02161  
R:Bernstein, K.E.; Alexander, C.B.; Mage, R.G.  
Immunogenetics 18, 387-397, 1983  
A>Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplot  
A:Reference number: A91749; MUID:84030930; PMID:6113520  
A:Accession: A91749  
A:Molecule type: mRNA  
A:Residues: 1-323 <BER>  
A:Cross-references: UNIPROT:P01870  
A:Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr  
R:Pratt, D.M.; Mole, L.E.  
Biochem. J. 151, 337-349, 1975  
A>Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglob  
A:Reference number: A90290; MUID:76135469; PMID:1243651  
A:Accession: A90290  
A:Molecule type: protein  
A:Residues: 1-47, 'E', 49-71, 'PV', 72-128 <PRA>  
R:Matteens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.  
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982  
A>Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain  
A:Reference number: A93928; MUID:83299917; PMID:6193512  
A:Accession: A93928  
A:Molecule type: mRNA  
A:Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>  
A:Cross-references: GB:M16426; NID:9165111; PIDN:AAA51289.1; PID:9165112

A:Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker  
R:Fruhnter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.  
Biochem. J. 116, 249-259, 1970  
A>Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin C  
A:Reference number: A90245; MUID:70110015; PMID:5461106  
A:Accession: A90245  
A:Molecule type: protein  
A:Residues: 132-143, 'E', 145-161 <FRU>  
R:Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.  
in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell,  
A:Reference number: A94416  
A:Accession: A94416  
A:Molecule type: protein  
A:Residues: 129-131, 155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D', 202-217, 'E', 219-232, 'Q',  
A:Note: this has the e15 allotypic marker, 185-Ala  
C:Complex: An immunoglobulin heterodimer subunit consists of two identical light (kappa)  
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lat  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterodimer; heterotetramer; immunoglobulin  
F:20-82/Domain: immunoglobulin homology <IM1>  
F:130-199/Domain: immunoglobulin homology <IM2>  
F:236-303/Domain: immunoglobulin homology <IM3>  
F:173/Binding site: carbohydrate (Asn) (covalent) #status predicted  
  
Query Match 67.6%; Score 1192.5; DB 1; Length 323;  
Best Local Similarity 67.9%; Pred. No. 2.9e-75;  
Matches 222; Conservative 37; Mismatches 61; Indels 7; Gaps 2;  
  
Qy 4 KGPSVPLAPSSKSTGSGTAALGCLVKDYFPEPVYVSNNSGALTSQVHFPFPAVLQSSGLY 63  
Db 4 KAPSVPLAPCGDTPSPSTVTLGCLVKGYLPEPVYVSNNSGTLTNGVTFPFRVRSGLY 63  
Qy 64 SLSVSVTVSSSLGTQTYICNVNHRKSNTRKVDKVEPKSCDKHTHCPCPAPPELLGGPSV 123  
Db 64 SLSVSVTVSSS---QPTCNVAHPATNTKVDKVAPESTCSK---PCPPELLGGPSV 116  
Qy 124 FLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVNNVTKRPREQYNRY 183  
Db 117 FLFPPKPKDTLMISRTPEVTCVVDVSDDDPEVQFTVNNQVETAPPLLEQGFNST 176  
Qy 184 RVSVSLTVLHQWMMNKEKCKVSNKALPAPIEKITSKAKVQPREQVYVTLPPSRDELTK 243  
Db 177 RVSVSLTVLHQWMMNKEKCKVSNKALPAPIEKITSKAKVQPREQVYVTLPPSRDELTK 236  
Qy 244 NOVSLTCLVKGFYPSDIAVEWESNGQPEPNYKTPPVLDVSGSFYLLSKLTLDVSKRMQG 303  
Db 237 RSVSLTCLVIGYIPPIIHVEWESNGKAEEDNYKTPPAVLDSGSYFLYNKLSVPTSEWQRG 296  
Qy 304 NVFSGSVMEALHNHYQOQSLSLSPGK 330  
Db 297 DVFTCSVMEALHNHYQOQSLSLSPGK 323  
  
RESULT 13  
147161  
Ig gamma 3 chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: 147161  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A>Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s  
A:Reference number: 147158; MUID:95015845; PMID:7930579  
A:Accession: 147158  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: EMBL:U03781; NID:9433127; PIDN:AAA52219.1; PID:9433128  
A:Gene: IGG3  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IM3>

Query Match 67.4%; Score 1189; DB 2; Length 328;  
 Best Local Similarity 66.9%; Pred. No. 5.1e-75;  
 Matches 222; Conservative 43; Mismatches 61; Indels 6; Gaps 3;

1 ASTKSPVPLPASPSSKSTSGGTAALGCLVKQVFPBPVTVSNMNSGALTSGVHFPFPAVLQSS 60  
 1 AKPTAPSVPLPASCGRDTSGRNVNAGCLASSTYFPEVTVTMNSGALTSGVHFPFPAVLQSS 60

61 GLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDTHTCPCPAPPELLLGG 120  
 61 GLYSLSVTVTPASSLSKSKSYCNVNHATTKTKVDRKQTKT---KPPCLPGCE-VAG 116

121 PSVFPPPKPKDMLTMSRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNVKTKPREQYN 180  
 117 PSVFPPPKPKDMLTMSRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNVKTKPREQYN 176

181 STYRVSVLTIVLHONMNGKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240  
 177 STYRVSVLPIQHOMLKGKFKCKCKVNNVDLPAPITRTISKAKVQPREQVYTLPPPAEE 236

241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTPPVLDVSGSFPLYSKLTVDKS 298  
 237 LSRKRVYTCVIGVYPPDIHVEWESNGQPREPGRYRTTPPOQDVDTFTFLYSKLAVDKA 296

299 RWQGNVFCSCVMEALHNHYOQRSLSLSPGK 330  
 297 RWDGTFECVAVMEALHNHYOQRSLSLSPGK 328

Db

## RESULT 14

G2GP

19 gamma-2 chain C region - guinea pig  
 C:Species: Cavia porcellus (guinea pig)  
 C:Date: 07-May-1981 #sequence revision 07-May-1981 #next change 03-Jul-2004  
 C:Accession: A94553; A90352; A90359; A90384; A90385; A02151

R:Titischmann, T.M.  
 submitted to the Aclae, April 1975

A:Reference number: A94553  
 A:Accession: A94553

A:Molecule type: protein  
 A:Residues: 1-3 <TRI>

A:Cross-references: UNIPROT:P01862  
 R:Bitshstein, B.K.; Hussain, Q.Z.; Cebra, J.J.

Biochemistry 10, 18-25, 1971

A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am  
 A:Reference number: A90352; MUID:71058471; PMID:5538606

A:Accession: A90352  
 A:Molecule type: protein

A:Residues: 4-68 <BIR>  
 R:Turner, K.J.; Cebra, J.J.

Biochemistry 10, 9-17, 1971

A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Am  
 A:Reference number: A90359; MUID:71058486; PMID:5538616

A:Accession: A90359  
 A:Molecule type: protein

A:Residues: 69-133.312-329 <TRR>  
 R:Tracey, D.E.; Cebra, J.J.

Biochemistry 13, 4796-4803, 1974

A:Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.  
 A:Reference number: A90384; MUID:75036072; PMID:4429665

A:Accession: A90384  
 A:Molecule type: protein

A:Residues: 134-226 <TRA>  
 R:Titischmann, T.M.; Cebra, J.J.

Biochemistry 13, 4804-4811, 1974

A:Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.  
 A:Reference number: A90385; MUID:75036073; PMID:4609467

A:Accession: A90385  
 A:Molecule type: protein

A:Residues: 227-311 <TR2>  
 R:Oliveira, B.; Lamm, M.E.

Biochemistry 10, 26-31, 1971

A:Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.

A:Reference number: A90354; MUID:71058474; PMID:4922544  
 A:Contents: annotation; disulfide bonds  
 A:Note: Cys-16 is involved in a heavy-light chain bond  
 C:Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (Lap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lat  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 F:21-81/Domain: immunoglobulin homology <IM1>  
 F:135-204/Domain: immunoglobulin homology <IM2>  
 F:241-310/Domain: immunoglobulin homology <IM3>  
 F:28-79/Disulfide bonds: #status experimental  
 F:142-202/Disulfide bonds: #status experimental  
 F:178/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:248-308/Disulfide bonds: #status experimental

Query Match 66.6%; Score 1174.5; DB 1; Length 329;  
 Best Local Similarity 68.2%; Pred. No. 5.2e-74;  
 Matches 227; Conservative 31; Mismatches 66; Indels 9; Gaps 4;

1 ASTKSPVPLPASPSSKSTSGGTAALGCLVKQVFPBPVTVSNMNSGALTSGVHFPFPAVLQSS 60  
 2 AKTTAPSVPLPAAACVDTSGSMNTLGLVKGYFPEVTVKMSGALTSGVHFPFPAVLQ-S 60

61 GLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDTH--TCPPCAPELL 118  
 61 GLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDTH--TCPPCAPELL 116

119 GGPVPLFPKPKDMLTMSRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNVKTKPREQ 178  
 117 GGPVPLFPKPKDMLTMSRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNVKTKPREQ 176

179 YNSTRVSVLTIVLHONMNGKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSR 238  
 177 YNSTRVSVLTIVLHONMNGKCKVSNKALPAPIEKTISKAKVQPREQVYTLPPSR 236

239 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTPPVLDVSGSFPLYSKLTVD 296  
 237 DELSKSKVSVTCLINFPFADIHVMANRNPVVSKEKKNPPIIDAGSYLYSKLTVD 296

297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329  
 297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329

297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329  
 297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329

297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329  
 297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329

297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329  
 297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329

297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329  
 297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329

297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329  
 297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329

297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329  
 297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329

297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329  
 297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329

297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329  
 297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329

297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329  
 297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329

297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329  
 297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329

297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329  
 297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329

297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329  
 297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329

297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329  
 297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329

297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329  
 297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329

297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329  
 297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329

297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329  
 297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329

297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329  
 297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329

297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329  
 297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329

297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329  
 297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329

297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329  
 297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329

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 297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329

297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329  
 297 KSRWQGNVFCSCVMEALHNHYOQRSLSLSPG 329

```
Db      202 GLYSLSVVTVPASTSGAQTFCNVAHPASSTKVDKRVEPGCPDPECKHC-RCPPPELPPG 260
Qy      121 PSVFLFPPPKXDITLMIISRTPEVTCVVVDVSHEDPEVKFNNVYDGVENVHNKTKPREEQYN 180
Db      261 PSVFLFPPPKXDITLISGTPEVTCVVVDVGDDPEVQFSMFVDNVEVRTARTKPREEQFN 320
Qy      181 STYRVVSVLTUHLQWMMNGKEFKCKVSNKALPAPIEKTIISKAKVQPREPQVYTLPPSRDE 240
Db      321 STFRVVSALPQIHODMTGGEFKCKVHNALPAPIVRTISRTKGQAREPQVYVLAAPQEE 380
Qy      241 LTKNOVSLTCLYKGFYPSDIAVEMESNGOP--ENNYKTPVYLDVSGSFELYSKLTVDKS 298
Db      381 LSKSTLSVTCLVTGFYPDYIAVEMQKNGQPESEBDKIGTTSQLDADGSTFLYSRLRVDRN 440
Qy      299 RWOQGNVFSCSVMEHALNHNHYOQRSLSLSPGX 330
Db      441 SWQEGDITYACVVMHEALNHNHYTQKSISKPPGX 472
```

Search completed: June 7, 2005, 09:02:33  
Job time : 35.7668 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: June 7, 2005, 08:39:41 ; Search time 162.435 Seconds  
(without alignments)  
1040.329 Million cell updates/sec

Title: US-10-000-439-2

Perfect score: 1764

Sequence: 1 ASTKGPSVFPPLAPSSKSTSG.....MHEALHNHYQSRSLSPGK 330

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1729	98.0	330	1 GCI_HUMAN	P01857 homo sapien
2	1729	98.0	465	2 Q6GMX6	Q6GMX6 homo sapien
3	1729	98.0	469	2 Q7ZRP5	Q7ZRP5 homo sapien
4	1729	98.0	470	2 Q6PJA4	Q6PJA4 homo sapien
5	1729	98.0	470	2 Q7ZSW1	Q7ZSW1 homo sapien
6	1729	98.0	475	2 Q6GMW7	Q6GMW7 homo sapien
7	1729	98.0	476	2 Q6GMX1	Q6GMX1 homo sapien
8	1726	97.8	466	2 Q6IN78	Q6IN78 homo sapien
9	1726	97.8	472	2 Q6N089	Q6N089 homo sapien
10	1725	97.8	473	2 Q6P055	Q6P055 homo sapien
11	1725	97.8	475	2 Q6M2Q6	Q6M2Q6 homo sapien
12	1725	97.8	480	2 Q6N094	Q6N094 homo sapien
13	1725	97.8	481	2 Q6N097	Q6N097 homo sapien
14	1725	97.8	482	2 Q7Z351	Q7Z351 homo sapien
15	1722	97.6	466	2 Q6N096	Q6N096 homo sapien
16	1720	97.5	348	2 Q6PYX1	Q6PYX1 homo sapien
17	1720	97.5	478	2 Q6P181	Q6P181 homo sapien
18	1720	97.5	480	2 Q6P0F1	Q6P0F1 homo sapien
19	1718	97.4	475	2 Q6N095	Q6N095 homo sapien
20	1718	97.4	544	2 Q6P0J5	Q6P0J5 homo sapien
21	1710	96.9	473	2 Q6M2V7	Q6M2V7 homo sapien
22	1592.5	90.3	518	2 Q6N030	Q6N030 homo sapien
23	1588.5	90.1	521	2 Q6N4Y9	Q6N4Y9 homo sapien
24	1577.5	89.4	509	2 Q8N2P17	Q8N2P17 homo sapien
25	1566	88.8	326	1 GC2_HUMAN	P01859 homo sapien
26	1566	88.8	417	2 Q6N093	Q6N093 homo sapien
27	1561	88.5	465	2 Q6P0C4	Q6P0C4 homo sapien
28	1552.5	88.0	327	1 GC4_HUMAN	P01861 homo sapien
29	1552.5	88.0	473	2 Q8TC63	Q8TC63 homo sapien
30	1552	88.0	493	2 Q68CN4	Q68CN4 homo sapien
31	1551	87.9	464	2 Q6M2U6	Q6M2U6 homo sapien

32	1543.5	87.5	476	2 Q6MZX7	Q6MZX7 homo sapien
33	1486.5	84.3	354	2 Q86T2	Q86T2 homo sapien
34	1228.5	69.6	337	2 Q95M34	Q95M34 equus caball
35	1226	69.5	679	2 Q96P08	Q96P08 homo sapien
36	1210.5	68.6	487	2 Q65ZL2	Q65ZL2 mus sp. fv/
37	1192.5	67.6	323	1 GC_RABIT	P01870 oryctolagus
38	1174.5	66.6	329	1 GC2_CAVPO	P01862 cavia porce
39	1128	63.9	290	1 GC3_HUMAN	P01860 homo sapien
40	1117.5	63.4	333	1 GCB_RAT	P20761 rattus norv
41	1117	63.3	463	2 Q99LC4	Q99LC4 mus musculu
42	1116	63.3	458	2 Q65Z01	Q65Z01 homo sapien
43	1114	63.2	326	1 GCI_RAT	P20759 rattus norv
44	1110	62.9	470	2 Q7TMK1	Q7TMK1 mus musculu
45	1109	62.9	324	1 GCI_MOUSE	P01868 mus musculu

#### ALIGNMENTS

RESULT 1	ID	GCI_HUMAN	STANDARD;	PRT;	330 AA.
AC	P01857;				
DT	21-JUL-1986 (rel. 01, Created)				
DT	21-JUL-1986 (rel. 01, Last sequence update)				
DT	25-OCT-2004 (rel. 45, Last annotation update)				
DE	IG gamma-1 chain C region.				
OS	Name=IGHG1;				
GN	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=82274238; PubMed=6287432;				
RA	Ellison J.W., Berson B.J., Hood L.B.;				
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene.";				
RL	Nucleic Acids Res. 10:4071-4079(1982).				
RN	[2]				
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).				
RX	MEDLINE=71064024; PubMed=5489771;				
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,				
RT	Waxdal M.J., Edelman G.M.;				
RL	acid sequence of heavy-chain cyanogen bromide fragments HI-H4.";				
RN	Biochemistry 9:3161-3170(1970).				
RP	SEQUENCE OF 136-329 (EU).				
RX	MEDLINE=71064025; PubMed=5530842;				
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,				
RT	Edelman G.M.;				
RL	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";				
RN	Biochemistry 9:3171-3181(1970).				
RP	[4]				
RX	SEQUENCE (MYELOMA PROTEIN NIE).				
RA	MEDLINE=77070269; PubMed=826475;				
RT	Ponstingl H., Hilschmann N.;				
RL	"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";				
RN	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).				
RP	[5]				
RX	SEQUENCE (MYELOMA PROTEIN KOL) AND DISULFIDE BONDS.				
RA	MEDLINE=83289131; PubMed=6884994;				
RT	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;				
RL	"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";				
RN	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).				
RP	[6]				
RX	DISULFIDE BONDS.				
RA	MEDLINE=71064027; PubMed=4923144;				

RA Gali W.E., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. X.  
RL Intrachain disulfide bonds."  
RN Biochemistry 9:3188-3196(1970).  
RX [7]  
RP DISULFIDE BONDS.  
RX MEDLINE=77070267; PubMed=1002129;  
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal  
RT IgG1 immunoglobulin (myeloma protein N1e), I: purification and  
RT characterization of the protein, the L- and H-chains, the cyanogen  
RT bromide cleavage products, and the disulfide bridges."  
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
RM [8]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
RX MEDLINE=81208100; PubMed=7236608;  
RA Deisenhofer J.;  
RT "Crystallographic refinement and atomic models of a human Fc fragment  
RT and its complex with fragment B of protein A from Staphylococcus  
RT aureus at 2.9- and 2.8-A resolution."  
RN Biochemistry 20:2361-2370(1981).  
CC -1- MISCELLANEOUS: N1e has the G1M(17) allotypic marker, 97-K, and the  
CC G1M(1) markers, 239-D and 241-L. KOL and EU sequences have the  
CC G1M(3) marker and the G1M (non-1) markers.  
CC -1- MISCELLANEOUS: N1e also differs in the amidation states of 35,  
CC 116, 198, 269 and 272.  
CC -1- MISCELLANEOUS: EU also differs in the amidation states of residues  
CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues  
CC 268-272.  
CC -1- MISCELLANEOUS: KOL also differs in the amidation states of  
CC residues 198, 267 and 272.  
-----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
CC EMBL: J00228; AAC82527.1; ALT\_INIT.  
-----  
DR PIR: A93433; GHU.  
DR PDB: 1A77; X-ray; H=1-103.  
DR PDB: 1D5B; X-ray; B/H=1-101.  
DR PDB: 1D5I; X-ray; H=1-101.  
DR PDB: 1DN2; X-ray; A/B=120-326.  
DR PDB: 1E4K; X-ray; A/B=106-329.  
DR PDB: 1FC1; X-ray; A/B=106-329.  
DR PDB: 1FC2; X-ray; D=106-329.  
DR PDB: 1FC3; X-ray; A=121-326.  
DR PDB: 1H2H; X-ray; H/K=1-330.  
DR PDB: 1I7Z; X-ray; B/D=1-103.  
DR PDB: 1IIS; X-ray; A/B=107-330.  
DR PDB: 1IIX; X-ray; A/B=107-330.  
DR PDB: 1I6X; X-ray; A=120-326.  
DR PDB: 1OQX; X-ray; A/B=119-350.  
DR PDB: 2RCS; X-ray; H=1-103.  
DR Genew; HGNC:5525; IGHG1.  
DR MIM: 147100; -.  
DR GO: GO:0005624; C:membrane fraction; NAS.  
DR GO: GO:0003823; F:antigen binding; TAS.  
DR GO: GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig\_1ike.  
DR InterPro; IPR003006; Ig\_1ike.  
DR Pfam; PF00047; Ig\_3.  
DR PROSITE; PS50835; IG\_LIKE; 3.  
DR PROSITE; PS50290; IG\_MHC; 2.  
KW 3D-structure; Direct protein sequencing; Glycoprotein;  
KW Immunoglobulin C region; Immunoglobulin domain.  
FT NON TER 1 98 CH1.  
FT DOMAIN 99 110 Hinge.  
FT

FT DOMAIN 111 223 CH2.  
FT DOMAIN 224 330 CH3.  
FT DISULFID 27 83 Interchain (with light chain).  
FT DISULFID 103 103 Interchain (with heavy chain).  
FT DISULFID 109 109 Interchain (with heavy chain).  
FT DISULFID 112 112 Interchain (with heavy chain).  
FT DISULFID 144 204  
FT DISULFID 250 308  
FT CARBOHYD 180  
FT VARIANT 97  
FT VARIANT 239  
FT VARIANT 241  
FT STRAND 23 24  
FT STRAND 26 33  
FT STRAND 38 38  
FT STRAND 41 41  
FT TURN 42 45  
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FT STRAND 57 58  
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FT STRAND 62 71  
FT HELIX 73 75  
FT TURN 76 78  
FT STRAND 82 87  
FT TURN 88 91  
FT STRAND 92 97  
FT TURN 102 103  
FT STRAND 122 126  
FT HELIX 130 134  
FT TURN 136 137  
FT STRAND 141 149  
FT STRAND 157 162  
FT TURN 163 164  
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FT HELIX 193 197  
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FT STRAND 215 219  
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FT STRAND 230 232  
FT HELIX 238 242  
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FT HELIX 297 301  
FT TURN 302 303  
FT STRAND 306 311  
FT TURN 313 314  
FT HELIX 316 318  
FT STRAND 319 324  
SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA3D CRC64;  
Query Match 98.0%; Score 1729; DB 1; Length 330;  
Best Local Similarity 97.9%; Pred. No. 3e-118;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 ASTKGPVFPPLAPSSKSTSGTALGCLVKDYFPEPTVNSMNSGALTSGVHTFPAVLQSS 60  
DB 1 ASTKGPVFPPLAPSSKSTSGTALGCLVKDYFPEPTVNSMNSGALTSGVHTFPAVLQSS 60

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QY 61 GLYSSSVVTVVPSSSLGTQTYICNVNHNKPSNTKVDKVPKSCDTHHTCPCPAPABELLGG 120
DB 61 GLYSSSVVTVVPSSSLGTQTYICNVNHNKPSNTKVDKVPKSCDTHHTCPCPAPABELLGG 120
QY 121 PSVFLFPPPKPDKDTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRREEQYN 180
DB 121 PSVFLFPPPKPDKDTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRREEQYN 180
QY 181 STYRVSVVLTVLHQMNGKKEYCKVKSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
DB 181 STYRVSVVLTVLHQMNGKKEYCKVKSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
QY 241 LTKNOVSLTCLVKGYPSPDIAVWESNQGPNNNYKTPPVLDSVGSFFLYSKLTVDKSRW 300
DB 241 LTKNOVSLTCLVKGYPSPDIAVWESNQGPNNNYKTPPVLDSVGSFFLYSKLTVDKSRW 300
QY 301 QCGNVFSCSVMHGALHNHYQKSLSPCK 330
DB 301 QCGNVFSCSVMHGALHNHYQKSLSPCK 330

RESULT 2
Q6GMX6 PRELIMINARY; PRT; 465 AA.
AC 06GMX6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RA EMBL: BC073766; AAH73766.1; --
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF0047; Ig_4.
DR Pfam: PF00409; Ig_2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00407; IGC1; 3.
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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 98.0%; Score 1729; DB 2; Length 465;
Best Local Similarity 97.9%; Pred. No. 4,5e-116;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKSPVPLAPSSKSTSGGTAALGCIYKDYFEPVTVSNMNGALTSVHFFPAVLQSS 60
DB 136 ASTKSPVPLAPSSKSTSGGTAALGCIYKDYFEPVTVSNMNGALTSVHFFPAVLQSS 195
QY 61 GLYSSSVVTVVPSSSLGTQTYICNVNHNKPSNTKVDKVPKSCDTHHTCPCPAPABELLGG 120
DB 196 GLYSSSVVTVVPSSSLGTQTYICNVNHNKPSNTKVDKVPKSCDTHHTCPCPAPABELLGG 255
QY 121 PSVFLFPPPKPDKDTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRREEQYN 180
DB 256 PSVFLFPPPKPDKDTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRREEQYN 315
QY 181 STYRVSVVLTVLHQMNGKKEYCKVKSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
DB 316 STYRVSVVLTVLHQMNGKKEYCKVKSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 375
QY 241 LTKNOVSLTCLVKGYPSPDIAVWESNQGPNNNYKTPPVLDSVGSFFLYSKLTVDKSRW 300
DB 376 LTKNOVSLTCLVKGYPSPDIAVWESNQGPNNNYKTPPVLDSVGSFFLYSKLTVDKSRW 435
QY 301 QCGNVFSCSVMHGALHNHYQKSLSPCK 330
DB 436 QCGNVFSCSVMHGALHNHYQKSLSPCK 465

RESULT 3
Q7Z7P5 PRELIMINARY; PRT; 469 AA.
AC Q7Z7P5;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE IGHG1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN [2]
RP SEQUENCE FROM N.A.
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RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RL [2]  
RC TISSUE=FROM N.A.  
RA Strusberg R.;  
RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC053984; AAHS3984.1; -.  
DR HSP; P01857; 1H2H.  
DR InterPro; IPR007110; IG-1like.  
DR InterPro; IPR003597; IG\_C1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein  
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match 98.0%; Score 1729; DB 2; Length 470;  
Best Local Similarity 97.9%; Pred. No. 4.6e-118;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKPSVPLAPSSKSTSGTALGCLVKDYFPEPVVSNMGSALTSGVHTFPAVLQSS 60  
DB 141 ASTKPSVPLAPSSKSTSGTALGCLVKDYFPEPVVSNMGSALTSGVHTFPAVLQSS 200  
QY 61 GLYSLSVVTVSSSLGTQTYICNVNHRKSNLKVDKVEPKSCDKTHTCPCPAPPELLGG 120  
DB 201 GLYSLSVVTVSSSLGTQTYICNVNHRKSNLKVDKVEPKSCDKTHTCPCPAPPELLGG 260  
QY 121 PSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVGVNAAVTKKPREEQYN 180  
DB 261 PSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVGVNAAVTKKPREEQYN 320  
QY 181 STYRVSVLTVLHQWMNKGKEYKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240  
DB 321 STYRVSVLTVLHQWMNKGKEYKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 380  
QY 241 LTKNOVSLTCLVKGFPSPDIAVWESNQPENNYKTPPVLDVSGSFFLYSKLTIVDKSRW 300  
DB 381 LTKNOVSLTCLVKGFPSPDIAVWESNQPENNYKTPPVLDVSGSFFLYSKLTIVDKSRW 440  
QY 301 QOQNVFSCSVMEALHNHYQOQSLSLSPGK 330  
DB 441 QOQNVFSCSVMEALHNHYQOQSLSLSPGK 470

RESULT 6  
ID 06GMW7 PRELIMINARY; PRT; 475 AA.  
AC 06GMW7;  
DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euteria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;

RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=spleen;  
RA Strusberg R.;  
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073782; AAH73782.1; -.  
DR InterPro; IPR003597; IG.  
DR InterPro; IPR007110; IG-1like.  
DR InterPro; IPR003597; IG\_C1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00407; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 475 AA; 51987 MW; 2A1FE55D736860F8 CRC64;

Query Match 98.0%; Score 1729; DB 2; Length 475;  
Best Local Similarity 97.9%; Pred. No. 4.6e-118;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKPSVPLAPSSKSTSGTALGCLVKDYFPEPVVSNMGSALTSGVHTFPAVLQSS 60  
DB 146 ASTKPSVPLAPSSKSTSGTALGCLVKDYFPEPVVSNMGSALTSGVHTFPAVLQSS 205  
QY 61 GLYSLSVVTVSSSLGTQTYICNVNHRKSNLKVDKVEPKSCDKTHTCPCPAPPELLGG 120  
DB 206 GLYSLSVVTVSSSLGTQTYICNVNHRKSNLKVDKVEPKSCDKTHTCPCPAPPELLGG 265  
QY 121 PSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVGVNAAVTKKPREEQYN 180  
DB 266 PSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVGVNAAVTKKPREEQYN 325  
QY 181 STYRVSVLTVLHQWMNKGKEYKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240  
DB 326 STYRVSVLTVLHQWMNKGKEYKCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 385  
QY 241 LTKNOVSLTCLVKGFPSPDIAVWESNQPENNYKTPPVLDVSGSFFLYSKLTIVDKSRW 300

```
DB      386  LTKNOVSLTCLVKGYPSPDIAVEMESNGOPENNKTTPPVLDSDGSFPLYSKLTVDKSRM 445
QY      301  OQGNVFSQSVMEALHNHYQKSLSPGK 330
DB      446  OQGNVFSQSVMEALHNHYQKSLSPGK 475

RESULT 7
Q6GMX1  PRELIMINARY; PRT; 476 AA.
ID      06GMX1
AC      05-JUL-2004 (TREMBLrel. 27, Created)
DT      05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE      Hypothetical protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxId=9606;
[1]
SEQUENCE FROM N.A.
RP      TISSUE=Spleen;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
RA      White M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA      Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA      Jones S.J., Maira M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
RP      TISSUE=Spleen;
RA      Strausberg R.;
RA      Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DB      EMBL; BC073773; AAH7373.1; -.
DR      InterPro; IPR003599; Ig.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003597; Ig_C1.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_V.
DR      Pfam; PF07654; C1-sec; 3.
DR      Pfam; PF00047; Ig; 4.
DR      SMART; SM00407; Ig; 2.
DR      SMART; SM00407; Ig; 3.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PSS00835; IG_LIKE; 4.
DR      PROSITE; PSS00290; IG_MHC; UNKNOWN_2.
KW      Hypothetical protein.
SQ      SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match      98.0%; Score 1729; DB 2; Length 476;
Best Local Similarity 97.9%; Pred. No. 4,6e-118;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
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DB      207  GLYSLSVVTVFSSLSGTQTYICNVNHNKPSNTKVDKPEKSCDKTHTPCPAPPELLGG 266
QY      121  PSVFLPFPKPDITMISRTPEVTCVVDVSHEDPEKFNWYDGVVHNVKTKPREQYN 180
DB      267  PSVFLPFPKPDITMISRTPEVTCVVDVSHEDPEKFNWYDGVVHNVKTKPREQYN 326

QY      181  STYRVSVLTVLHOMWNGKEKCKVSKKALPAPTEKITSKAKQPREPQVYTTLPSPDE 240
DB      327  STYRVSVLTVLHOMWNGKEKCKVSKKALPAPTEKITSKAKQPREPQVYTTLPSPDE 386

QY      241  LTKNOVSLTCLVKGYPSPDIAVEMESNGOPENNKTTPPVLDSDGSFPLYSKLTVDKSRM 300
DB      387  LTKNOVSLTCLVKGYPSPDIAVEMESNGOPENNKTTPPVLDSDGSFPLYSKLTVDKSRM 446

QY      301  OQGNVFSQSVMEALHNHYQKSLSPGK 330
DB      447  OQGNVFSQSVMEALHNHYQKSLSPGK 476

RESULT 8
Q6IN78  PRELIMINARY; PRT; 466 AA.
ID      06IN78
AC      05-JUL-2004 (TREMBLrel. 27, Created)
DT      05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE      IGHG1 protein.
GN      Name=IGHG1;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxId=9606;
[1]
SEQUENCE FROM N.A.
RP      TISSUE=Peripheral Nervous System;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
RA      White M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA      Jones S.J., Maira M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
RP      TISSUE=Peripheral Nervous System;
RA      Strausberg R.;
RA      Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DB      EMBL; BC072419; AAH72419.1; -.
DR      HSSP; P01861; IADQ.
DR      InterPro; IPR003599; Ig.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003597; Ig_C1.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_V.
DR      Pfam; PF07654; C1-sec; 3.
DR      SMART; SM00407; Ig; 2.
DR      SMART; SM00406; IGV; 1.
DR      SMART; SM00406; IGV; 1.
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DR PROSITE: PS00835; IG\_LIKE; 4.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN 2.  
SQ SEQUENCE 466 AA; 50853 MW; 53EB0BCEDE81076E CRC64;

Query Match 97.8%; Score 1726; DB 2; Length 466;

Best Local Similarity 97.6%; Pred. No. 7,5e-118;

Matches 322; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

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QY 1 ASTKGPVPEPLAPSSKSTSGTAAIGCLVKDYFPEPVTVSNMNGALTSGVHFPVALQSS 60
DB 137 ASTKGPVPEPLAPSSKSTSGTAAIGCLVKDYFPEPVTVSNMNGALTSGVHFPVALQSS 196
QY 61 GLYSLSVTVTVSSSLGTQTYICNNHKKPSNTKVDKRPKSCDTHHTPCPCAPABELLG 120
DB 197 GLYSLSVTVTVSSSLGTQTYICNNHKKPSNTKVDKRPKSCDTHHTPCPCAPABELLG 256
QY 121 PSVFLPPPKKDTLMISRTPEVTCVAVDVSHEDPEVKFNMVYDGVVHNAKTKPREEOYN 180
DB 251 PSVFLPPPKKDTLMISRTPEVTCVAVDVSHEDPEVKFNMVYDGVVHNAKTKPREEOYN 316
QY 181 STYRVSVLTVLHQMNMNGKEYKCKVSNKALPAPIEKTISKAKQPREQVYTLPPSRDE 240
DB 317 STYRVSVLTVLHQMNMNGKEYKCKVSNKALPAPIEKTISKAKQPREQVYTLPPSRDE 376
QY 241 LTRKNVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDVSQSFFLYSKLTVDKSRW 300
DB 377 LTRKNVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDVSQSFFLYSKLTVDKSRW 436
QY 301 QQGNVFSCSVMHGALHNHYQKSLSPGK 330
DB 437 QQGNVFSCSVMHGALHNHYQKSLSPGK 466
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## RESULT 9

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Q6N089 PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp666P15220.
GN Name=DKFZp666P15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human CDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobio G., Han M., Wiemann S.;
RA Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BA640627; CAE45781.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-secl; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
DR Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;
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Query Match 97.8%; Score 1726; DB 2; Length 472;  
Best Local Similarity 97.6%; Pred. No. 7,6e-118;  
Matches 322; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

```
QY 1 ASTKGPVPEPLAPSSKSTSGTAAIGCLVKDYFPEPVTVSNMNGALTSGVHFPVALQSS 60
DB 143 ASTKGPVPEPLAPSSKSTSGTAAIGCLVKDYFPEPVTVSNMNGALTSGVHFPVALQSS 202
QY 61 GLYSLSVTVTVSSSLGTQTYICNNHKKPSNTKVDKRPKSCDTHHTPCPCAPABELLG 120
DB 203 GLYSLSVTVTVSSSLGTQTYICNNHKKPSNTKVDKRPKSCDTHHTPCPCAPABELLG 262
QY 121 PSVFLPPPKKDTLMISRTPEVTCVAVDVSHEDPEVKFNMVYDGVVHNAKTKPREEOYN 180
DB 263 PSVFLPPPKKDTLMISRTPEVTCVAVDVSHEDPEVKFNMVYDGVVHNAKTKPREEOYN 322
QY 181 STYRVSVLTVLHQMNMNGKEYKCKVSNKALPAPIEKTISKAKQPREQVYTLPPSRDE 240
DB 323 STYRVSVLTVLHQMNMNGKEYKCKVSNKALPAPIEKTISKAKQPREQVYTLPPSRDE 382
QY 241 LTRKNVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDVSQSFFLYSKLTVDKSRW 300
DB 383 LTRKNVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDVSQSFFLYSKLTVDKSRW 442
QY 301 QQGNVFSCSVMHGALHNHYQKSLSPGK 330
DB 443 QQGNVFSCSVMHGALHNHYQKSLSPGK 472
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## RESULT 10

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Q6P055 PRELIMINARY; PRT; 473 AA.
ID Q6P055;
AC Q6P055;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Murny D.M., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.U., Ustin I.B., Toshnyuk S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Goughwood J., Green E.D., Dickson M.C.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RA Submitted (Jan-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065820; AAH65820.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
```

DR Pfam: PF07654; Cl-set: 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IG; 1.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;

Query Match 97.8%; Score 1725; DB 2; Length 473;  
Best Local Similarity 97.6%; Pred. No. 9e-118;  
Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ASTKPSVFPLPASPSSKSTSGGTAALGCLVKDYFPEPVVYSNMSGALTSGVHFFPAVLQSS 60  
DB 144 ASTKPSVFPLPASPSSKSTSGGTAALGCLVKDYFPEPVVYSNMSGALTSGVHFFPAVLQSS 203

QY 61 GLYSLSVVTVVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDRTHTCPCPAPABELLG 120  
DB 204 GLYSLSVVTVVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDRTHTCPCPAPABELLG 263

QY 121 PSVFLPPEPKDITLMSRTPEVTCVVVDVSHEDPEVKFMNYYDGVVHNNAKTKPREEQYN 180  
DB 264 PSVFLPPEPKDITLMSRTPEVTCVVVDVSHEDPEVKFMNYYDGVVHNNAKTKPREEQYN 323

QY 181 STYRVVSVLTVLHQMNGKEKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240  
DB 324 STYRVVSVLTVLHQMNGKEKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 383

QY 241 LTKNQSITCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSVGSFFLYSKLTVDKSRW 300  
DB 384 LTKNQSITCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSVGSFFLYSKLTVDKSRW 443

QY 301 QQGNVFSCSVHMEALHNHYQQRSLSLSPGK 330  
DB 444 QQGNVFSCSVHMEALHNHYQQRSLSLSPGK 473

RESULT 11  
Q6MZQ6 PRELIMINARY; PRT; 475 AA.

AC Q6MZQ6  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DE Hypothetical protein DKFZp686g1190.  
GN Name=DKFZp686g1190;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human esophagus tumor;  
RG The German Human CDNA Consortium;  
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobbo G.,  
RA Han M., Wiemann S.;  
RL Submitted (Aug-2003) to the EMBL/Genbank/DBJ databases.  
DR EMBL; BX640947; CAE45972.1; -  
DR HSSP; P01861; IADO.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003597; IG\_C1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IG; 1.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match 97.8%; Score 1725; DB 2; Length 475;  
Best Local Similarity 97.6%; Pred. No. 9e-118;  
Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ASTKPSVFPLPASPSSKSTSGGTAALGCLVKDYFPEPVVYSNMSGALTSGVHFFPAVLQSS 60  
DB 146 ASTKPSVFPLPASPSSKSTSGGTAALGCLVKDYFPEPVVYSNMSGALTSGVHFFPAVLQSS 205

QY 61 GLYSLSVVTVVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDRTHTCPCPAPABELLG 120  
DB 206 GLYSLSVVTVVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDRTHTCPCPAPABELLG 265

QY 121 PSVFLPPEPKDITLMSRTPEVTCVVVDVSHEDPEVKFMNYYDGVVHNNAKTKPREEQYN 180  
DB 266 PSVFLPPEPKDITLMSRTPEVTCVVVDVSHEDPEVKFMNYYDGVVHNNAKTKPREEQYN 325

QY 181 STYRVVSVLTVLHQMNGKEKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240  
DB 326 STYRVVSVLTVLHQMNGKEKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 385

QY 241 LTKNQSITCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSVGSFFLYSKLTVDKSRW 300  
DB 386 LTKNQSITCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSVGSFFLYSKLTVDKSRW 445

QY 301 QQGNVFSCSVHMEALHNHYQQRSLSLSPGK 330  
DB 446 QQGNVFSCSVHMEALHNHYQQRSLSLSPGK 475

RESULT 12  
Q6N094 PRELIMINARY; PRT; 480 AA.

AC Q6N094  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686o01196.  
GN Name=DKFZp686o01196;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human esophagus tumor;  
RG The German Human CDNA Consortium;  
RA Wandt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobbo G., Han M., Wiemann S.;  
RL Submitted (Aug-2003) to the EMBL/Genbank/DBJ databases.  
DR EMBL; BX640622; CAE45776.1; -  
DR HSSP; P01861; IADO.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003597; IG\_C1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IG; 1.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;

Query Match 97.8%; Score 1725; DB 2; Length 480;  
Best Local Similarity 97.6%; Pred. No. 9.2e-118;  
Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ASTKPSVFPLPASPSSKSTSGGTAALGCLVKDYFPEPVVYSNMSGALTSGVHFFPAVLQSS 60  
DB 151 ASTKPSVFPLPASPSSKSTSGGTAALGCLVKDYFPEPVVYSNMSGALTSGVHFFPAVLQSS 210

```
QY 61 GLYSLSVVTVSSSLGTQTYICNVNHNKSNTKVDKVEPKSCDKHTHTCPCPAPELLGG 120
DB 211 GLYSLSVVTVSSSLGTQTYICNVNHNKSNTKVDKVEPKSCDKHTHTCPCPAPELLGG 270
QY 121 PSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFWMYVDGVEVNAVNTKPRREOYN 180
DB 271 PSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFWMYVDGVEVNAVNTKPRREOYN 330
QY 181 STYRVVSVLTVLHQMNMNGKEYKCKVSNKALPAPIEKTIISKAKVOPREPOVYTLPPSRDE 240
DB 331 STYRVVSVLTVLHQMNMNGKEYKCKVSNKALPAPIEKTIISKAKVOPREPOVYTLPPSRDE 390
QY 241 LTRKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW 300
DB 391 LTRKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW 450
QY 301 OQGNVFCSCVMHEALHNHYQORSLSLSPGK 330
DB 451 OQGNVFCSCVMHEALHNHYQORSLSLSPGK 480

RESULT 13
Q6N097 PRELIMINARY; PRT; 481 AA.
AC Q6N097;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686H20196.
OS Homo sapiens (Human).
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominda; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wambner R., Heubner D., Mewes H.W., Well B., Amid C., Osanger A.,
RA Fob G., Han M., Wiemann S.,
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640619; CAB45773.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003199; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; Ig_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52759 MW; 47220D9E64BDP98B CRC64;

Query Match 97.8%; Score 1725; DB 2; Length 481;
Best Local Similarity 97.6%; Pred. No. 9.2e-118;
Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

1 ASTKGSVPLPSSKSTSGTAAAGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 60
152 ASTKGSVPLPSSKSTSGTAAAGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 211
QY 61 GLYSLSVVTVSSSLGTQTYICNVNHNKSNTKVDKVEPKSCDKHTHTCPCPAPELLGG 120
DB 212 GLYSLSVVTVSSSLGTQTYICNVNHNKSNTKVDKVEPKSCDKHTHTCPCPAPELLGG 271
QY 121 PSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFWMYVDGVEVNAVNTKPRREOYN 180
DB 272 PSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFWMYVDGVEVNAVNTKPRREOYN 331
```

```
QY 181 STYRVVSVLTVLHQMNMNGKEYKCKVSNKALPAPIEKTIISKAKVOPREPOVYTLPPSRDE 240
DB 332 STYRVVSVLTVLHQMNMNGKEYKCKVSNKALPAPIEKTIISKAKVOPREPOVYTLPPSRDE 391
QY 241 LTRKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW 300
DB 392 LTRKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW 451
QY 301 OQGNVFCSCVMHEALHNHYQORSLSLSPGK 330
DB 452 OQGNVFCSCVMHEALHNHYQORSLSLSPGK 481

RESULT 14
Q72351 PRELIMINARY; PRT; 482 AA.
AC Q72351;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686N02209.
OS Homo sapiens (Human).
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominda; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG Bloecher H., Boecher M., Mewes H.W., Well B., Amid C., Osanger A.,
RA Fob G., Han M., Wiemann S.,
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538118; CAD98026.1; -.
DR HSSP; P01857; 1H2H.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 482 AA; 52852 MW; EDA75F1901D1A034 CRC64;

Query Match 97.8%; Score 1725; DB 2; Length 482;
Best Local Similarity 97.6%; Pred. No. 9.2e-118;
Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

1 ASTKGSVPLPSSKSTSGTAAAGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 60
153 ASTKGSVPLPSSKSTSGTAAAGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 212
QY 61 GLYSLSVVTVSSSLGTQTYICNVNHNKSNTKVDKVEPKSCDKHTHTCPCPAPELLGG 120
DB 213 GLYSLSVVTVSSSLGTQTYICNVNHNKSNTKVDKVEPKSCDKHTHTCPCPAPELLGG 272
QY 121 PSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFWMYVDGVEVNAVNTKPRREOYN 180
DB 273 PSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFWMYVDGVEVNAVNTKPRREOYN 332
QY 181 STYRVVSVLTVLHQMNMNGKEYKCKVSNKALPAPIEKTIISKAKVOPREPOVYTLPPSRDE 240
DB 333 STYRVVSVLTVLHQMNMNGKEYKCKVSNKALPAPIEKTIISKAKVOPREPOVYTLPPSRDE 392
QY 241 LTRKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW 300
DB 393 LTRKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW 452
QY 301 OQGNVFCSCVMHEALHNHYQORSLSLSPGK 330
DB 453 OQGNVFCSCVMHEALHNHYQORSLSLSPGK 482
```

## RESULT 15

06N096 PRELIMINARY: PRT: 466 AA.  
ID 06N096  
AC 06N096:  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein DKFZp686I15196.  
GN Name=DKFZp686I15196;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human esophagus tumor;  
RG The German Human cDNA Consortium;  
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fodor G., Han M., Wiemann S.,  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BX640620; CAB4574.1; -  
DR HSSP: P01861; IADQ.  
DR InterPro: IPR003559; IG.  
DR InterPro: IPR007110; IG-1like.  
DR InterPro: IPR003597; IG\_C1.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF07654; C1-set; 3.  
DR SMART: SM00409; IG; 2.  
DR SMART: SM00407; IGc1; 3.  
DR SMART: SM00406; IGv; 1.  
DR PROSITE: PS50835; IG\_LIKE; 4.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein  
SQ SEQUENCE 466 AA; 50926 MW; 01E91B748D6D57C4 CRC64;

Query Match 97.6%; Score 1722; DB 2; Length 466;  
Best Local Similarity 97.3%; Pred. No. 1.5e-117;

Matches 321; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 ASTKGPSPVPLAPSSKSTSGTALGCLVKDYFPPPVTVSNVSGALTSGVHTFPAVLQSS 60  
DB 137 ASTKGPSPVPLAPSSKSTSGTALGCLVKDYFPPPVTVSNVSGALTSGVHTFPAVLQSS 196  
QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKHTCTPCPAPAPLGG 120  
DB 197 GLYSLSVVTVPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKHTCTPCPAPAPLGG 256  
QY 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYVVGVEVHNAVTKKPREEQYN 180  
DB 257 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYVVGVEVHNAVTKKPREEQYN 316  
QY 181 STYRVVSVLTIVHQNMNNGEKYCKVSNKALPAPIEKTIISKAKVQPREPOVYITLPPSRDE 240  
DB 317 STYRVVSVLTIVHQNMNNGEKYCKVSNKALPAPIEKTIISKAKVQPREPOVYITLPPSRDE 376  
QY 241 LTKNOVSLTCLVKGFYPSDIAVEMESNGOPENNYKTPPVLDVSGSFLLYSKLTVDKSRW 300  
DB 377 LTKNOVSLTCLVKGFYPSDIAVEMESNGOPENNYKTPPVLDVSGSFLLYSKLTVDKSRW 436  
QY 301 QQGNVFSQSVMEALHNHYQORSLSLSPGK 330  
DB 437 QQGNVFSQSVMEALHNHYQORSLSLSPGK 466

Search completed: June 7, 2005, 09:01:27  
Job time : 165.435 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: June 7, 2005, 08:38:56 ; Search time 167.565 Seconds

(without alignments)  
761.681 Million cell updates/sec

Title: US-10-000-439-2

Perfect score: 1764  
Sequence: 1 ASTKCPVFPPLAPSSKSTSG.....MHEALHNHYQGRSLSPCK 330Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp19808:\*\n2: geneseqp19908:\*\n3: geneseqp20008:\*\n4: geneseqp20018:\*\n5: geneseqp20025:\*\n6: geneseqp20038:\*\n7: geneseqp20038:\*\n8: geneseqp20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1764	100.0	330	6	AAO19664 Human IgG
2	1729	98.0	330	4	AAAB04071 ZCytoc 10
3	1729	98.0	330	5	AAAB47856 Human Ig-
4	1729	98.0	330	5	AAE21960 Human dea
5	1729	98.0	330	5	ABB81641 Human IgG
6	1729	98.0	330	5	ABB05736 Human imm
7	1729	98.0	330	6	ABP71856 Human IgG
8	1729	98.0	330	6	AAE32915 Human imm
9	1729	98.0	330	6	AAE32627 Human imm
10	1729	98.0	330	6	ABR82103 Human DR6
11	1729	98.0	330	6	AAO31102 Human A2-
12	1729	98.0	330	6	ABR55836 Anti-Ang-
13	1729	98.0	330	6	AAO30893 Human imm
14	1729	98.0	330	7	ADP11389 Anti-OPGL
15	1729	98.0	330	7	ADP97351 Human IgG
16	1729	98.0	330	7	ADP83605 Cytokine
17	1729	98.0	330	7	ADP75001 Human Ig
18	1729	98.0	330	8	ADM41537 Anti-Inte
19	1729	98.0	330	8	ADM68911 Human IgG
20	1729	98.0	330	8	ADR43460 Heavy cha
21	1729	98.0	330	8	ADR31605 Human IgG
22	1729	98.0	330	8	ADP87909 Anti-IFN-
23	1729	98.0	330	8	ADN33230 IgG1-CH h
24	1729	98.0	330	8	ADP94906 Anti-IFN-
25	1729	98.0	332	8	ADL35095 Human IgG

26	1729	98.0	333	8	ADJ95912 Human IgG
27	1729	98.0	333	8	ADL22761 Human ant
28	1729	98.0	351	2	AAE43685 Human kap
29	1729	98.0	356	8	ADJ95976 Immunogl
30	1729	98.0	371	1	ADP91918 Sequence
31	1729	98.0	442	6	ABR39465 Humanised
32	1729	98.0	442	6	ABR39474 Humanised
33	1729	98.0	442	6	ABU08311 Humanised
34	1729	98.0	442	6	ABU08320 Humanised
35	1729	98.0	442	6	ABR39793 Humanised
36	1729	98.0	442	6	ABR80113 Deglycosy
37	1729	98.0	442	6	ABR80109 Heavy cha
38	1729	98.0	442	7	ADP94066 Humanised
39	1729	98.0	442	7	ADP94075 Humanised
40	1729	98.0	442	7	ADN61714 Humanised
41	1729	98.0	444	6	AAE35327 Humanised
42	1729	98.0	444	6	AAE34876 B1W4/8 a
43	1729	98.0	444	8	ADL15443 Humanised
44	1729	98.0	444	8	ADU00851 Humanised
45	1729	98.0	445	6	AAO31101 Human A2-

## ALIGNMENTS

RESULT 1	
AAO19664	
ID	AAO19664 standard; protein; 330 AA.
AC	AAO19664;
DT	28-MAR-2003 (first entry)
XX	
DE	Human IgG1 heavy chain constant region.
XX	
KW	Human; IgG1; immunoglobulin G; immunotherapy; immune disease;
KW	Fc epsilon receptor; autoimmune disease; constant region; heavy chain;
KW	antisthmatic; antiallergic; antiinflammatory; dermatological;
KW	antiasthmatic; antirheumatic; antidiabetic; neuroprotective.
OS	Homo sapiens.
XX	
PN	WO200288317-A2.
XX	
PD	07-NOV-2002.
XX	
PF	01-MAY-2002; 2002WO-US013527.
XX	
PR	01-MAY-2001; 2001US-00847208.
XX	
PR	24-OCT-2001; 2001US-00000439.
XX	
PA	(REGC ) UNIV CALIFORNIA.
XX	
PI	Saxon A, Zhang K, Zhu D;
XX	
DR	WPI; 2003-103456/09.
XX	
PT	New fusion molecules comprising polypeptide sequences that bind to IgG
PT	inhibitory receptor and native IgE receptor, useful for treating IgE-
PT	mediated hypersensitivity reactions, e.g. asthma or allergies, or
XX	autoimmune diseases.
PS	Claim 64; Fig 2; 116pp; English.
XX	
CC	The present invention relates to a fusion molecule comprising a first
CC	polypeptide sequence capable of specific binding to a native IgG
CC	inhibitory receptor consisting of an immune receptor tyrosine-based
CC	inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,
CC	functionally connected to a second polypeptide sequence capable of
CC	specific binding directly or indirectly to a native IgE receptor
CC	(Fc epsilonR). Also provided are nucleotide sequences encoding such a
CC	fusion protein. The fusion molecules and compositions are useful for
CC	treating an IgE-mediated biological response, preferably an IgE-mediated

CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic  
CC dermatitis, severe food allergies, chronic urticaria, angioedema or  
CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,  
CC type-1 diabetes mellitus, or multiple sclerosis, and for preventing of,  
CC or symptoms resulting from, a type I hypersensitivity reaction in a  
CC subject receiving immunotherapy. The present sequence is the human IgG1  
CC heavy chain constant region  
XX  
SQ Sequence 330 AA;  
Query Match 100.0%; Score 1764; DB 6; Length 330;  
Best Local Similarity 100.0%; Pred. No. 4e-125;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
DB 1 ASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
QY 61 GLYSLSVVTVPPSSSLGTQTYICNVNHRKSNTRVKDKVPEPKSCDKHTHTCPCPAPPELLGG 120  
DB 61 GLYSLSVVTVPPSSSLGTQTYICNVNHRKSNTRVKDKVPEPKSCDKHTHTCPCPAPPELLGG 120  
QY 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFWMYDGVVHNVKTTPREEQYN 180  
DB 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFWMYDGVVHNVKTTPREEQYN 180  
QY 181 STYRVVSVLTVLHQMNGEKYCKVSNKALPAPIEKTTSKAKVQPREQVYTLTPPSRDE 240  
DB 181 STYRVVSVLTVLHQMNGEKYCKVSNKALPAPIEKTTSKAKVQPREQVYTLTPPSRDE 240  
QY 241 LRKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDVSGSFPLYSKLTVDKSRW 300  
DB 241 LRKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDVSGSFPLYSKLTVDKSRW 300  
QY 301 QOQNVFSCVMHEALHNHYQOQSLSLSPGK 330  
DB 301 QOQNVFSCVMHEALHNHYQOQSLSLSPGK 330  
RESULT 2  
AAB04071 ID AAB04071 standard; protein; 330 AA.  
XX AAB04071;  
DT 11-APR-2001 (first entry)  
XX Zcyfor 10::Igg gamma fusion peptide.  
DE Zcyfor 10::Igg gamma fusion peptide.  
XX zcyfor 10 cytokine receptor; cytokine; receptor; antibody; ligand;  
KM binding; detection; modulation; recombinant cell; haematopoietic cell;  
KW lymphoid cell; myeloid cell; lymph; immune system; blood; bone;  
XX inflammatory response; inflammation; spleen; human.  
OS Synthetic.  
OS Homo sapiens.  
PN WO200068381-A1.  
XX 16-NOV-2000.  
XX 11-MAY-2000; 2000MO-US012924.  
XX PF 11-MAY-1999; 99US-00309861.  
XX PR 11-MAY-1999; 99US-00309861.  
XX PA (ZYMO ) ZYMOGENETICS INC.  
XX PI Presnell SR, Foster DC, Hammond AK, Lok S;  
XX WPI; 2001-016096/02.  
XX DR N-PSDB; AAA54473.  
XX PT New cytokine receptor mouse zcyfor 10, useful for detecting ligands that

PT stimulate proliferation or development of hematopoietic, lymphoid and  
PT myeloid cells.  
XX Example 17; Page 120-121; 134pp; English.  
XX Isolating a nucleotide which encodes the zcyfor 10 cytokine receptor  
CC enables the production of recombinant cells expressing the receptor.  
CC Those cells can then be used to detect the presence of a modulator of  
CC zcyfor10 protein by culturing the cells in the presence of a test ligand  
CC and comparing levels of activity of mouse zcyfor10 in the presence and  
CC absence of the test sample. Similarly, detection of zcyfor10 receptor  
CC ligand within a test sample can be achieved. The method comprising  
CC contacting a test sample containing an amino acid sequence from Cys45 or  
CC Gly25 to Pro230 of the zcyfor 10 cytokine receptor and detecting the  
CC binding of the polypeptide to a ligand in the sample. Specified peptide  
CC fragments of the zcyfor 10 cytokine receptor and the methods described  
CC are used to identify ligands that stimulate the proliferation and/or  
CC development of hematopoietic, lymphoid and myeloid cells. Peptide  
CC fragments of the cytokine receptor are useful for treating lymphoid,  
CC immune, inflammatory, splenic, blood or bone disorders and for generating  
CC antibodies directed against the receptor. A vector expressing a secreted  
CC human zcyfor 10 heterodimer is constructed. In this construct the  
CC extracellular cytokine binding domain of zcyfor 10 is fused to the heavy  
CC chain of IgG gamma and the extracellular portion of the the heteromeric  
CC cytokine receptor subunit (an interleukin receptor subunit) is fused to  
CC human kappa light chain (See GENESEQ record AAA54474). The two sequences  
CC are fused together using two primers (AAA54475, AAA54476)  
XX  
SQ Sequence 330 AA;  
Query Match 98.0%; Score 1729; DB 4; Length 330;  
Best Local Similarity 97.9%; Pred. No. 1.8e-122;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 ASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
DB 1 ASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
QY 61 GLYSLSVVTVPPSSSLGTQTYICNVNHRKSNTRVKDKVPEPKSCDKHTHTCPCPAPPELLGG 120  
DB 61 GLYSLSVVTVPPSSSLGTQTYICNVNHRKSNTRVKDKVPEPKSCDKHTHTCPCPAPPELLGG 120  
QY 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFWMYDGVVHNVKTTPREEQYN 180  
DB 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFWMYDGVVHNVKTTPREEQYN 180  
QY 181 STYRVVSVLTVLHQMNGEKYCKVSNKALPAPIEKTTSKAKVQPREQVYTLTPPSRDE 240  
DB 181 STYRVVSVLTVLHQMNGEKYCKVSNKALPAPIEKTTSKAKVQPREQVYTLTPPSRDE 240  
QY 241 LRKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDVSGSFPLYSKLTVDKSRW 300  
DB 241 LRKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDVSGSFPLYSKLTVDKSRW 300  
QY 301 QOQNVFSCVMHEALHNHYQOQSLSLSPGK 330  
DB 301 QOQNVFSCVMHEALHNHYQOQSLSLSPGK 330  
RESULT 3  
AAM47856 ID AAM47856 standard; protein; 330 AA.  
XX AAM47856;  
XX 22-FEB-2002 (first entry)  
XX Human Ig-gamma1 heavy chain constant region amino acid sequence.  
XX Human; immunoadhesin; intercellular adhesion molecule; ICAM-1;  
KW human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold;  
XX transgenic plant.  
XX





CC recuperation from chemotherapy, recuperation from irradiation therapy, or  
CC a condition or symptom related to the above mentioned diseases in a  
CC mammal. The present sequence is human DR6 protein-related protein  
XX  
SQ Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 5; Length 330;  
Best Local Similarity 97.9%; Pred. No. 1.8e-122;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKPSVPLPSSKSTSGTAAAGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
DB 1 ASTKPSVPLPSSKSTSGTAAAGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
QY 61 GLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHPCPCPAPELLGG 120  
DB 61 GLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHPCPCPAPELLGG 120  
QY 121 PSVFLPPEPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVVHNNAKTRPEEQYN 180  
DB 121 PSVFLPPEPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVVHNNAKTRPEEQYN 180  
QY 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240  
DB 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240  
QY 241 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300  
DB 241 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300  
QY 301 QOQNVFSCSVMHGALHNHYTQKSLSLSPGK 330  
DB 301 QOQNVFSCSVMHGALHNHYTQKSLSLSPGK 330

RESULT 5  
ABB81641  
ID ABB81641 standard; protein; 330 AA.

AC ABB81641;  
XX  
DT 25-SEP-2002 (first entry)

DE Human IgG gamma 1 heavy chain SEQ ID NO:15.

XX Human; zcytor19; cytokine receptor; immunosuppressive; cytosolatic;  
XX antirheumatic; antiarthritic; neuroprotective; anti-inflammatory;  
XX antidiabetic; nephrotoxic; dermatological; anti-HIV; haemostatic;  
XX vaccine; immune system; T-cell specific leukemia; lymphoma; lupus;  
XX autoimmune disease; inflammatory bowel disease; Crohn's disease; asthma;  
XX diabetes mellitus; inflammatory bowel disease; Crohn's disease; asthma;  
XX immunologic renal disease; glomerulonephritis; vasculitis; polyarteritis;  
XX mesangiolipidiferative disease; chronic lymphocytic leukaemia; bronchitis;  
XX secondary glomerulonephritis; scleroderma; amyloidosis; multiple myeloma;  
XX haemolytic uraemic syndrome; renal neoplasm; urological neoplasm;  
XX emphysema; chronic airway disease.

OS Homo sapiens.

PN WO200244209-A2.

PD 06-JUN-2002.

PF 28-NOV-2001; 2001WO-US044808.

PR 28-NOV-2000; 2000US-0253561P.

PR 07-FEB-2001; 2001US-0267211P.

XX (ZYMO ) ZYMOGENETICS INC.

XX Presnell SR, Xu W, Novak JE, Whitmore TE, Grant FJ;

XX WPI; 2002-527700/56.

DR N-PSDB; ABQ73076.

XX Novel Zcytor19 polypeptides and polynucleotides useful for stimulating  
PT immune responses in animals for producing antibodies, and for treating  
PT autoimmune diseases, leukemia and asthma.

PS Example 7; Page 171-172; 200pp; English.

XX The present invention describes an isolated human zcytor19 protein (I),  
CC and truncated zcytor19 proteins. (I) has immunosuppressive, cytosolatic,  
CC antirheumatic, antiarthritic, neuroprotective, anti-inflammatory,  
CC antidiabetic, nephrotoxic, dermatological, anti-HIV and haemostatic  
CC activities, and can be used in vaccines. (I) or an antibody binding (I)  
CC can be used for suppressing the immune system for reducing rejection of  
CC tissue or organ transplants and grafts and for treating T-cell specific  
CC leukaemias or lymphomas and autoimmune diseases including rheumatoid  
CC arthritis, multiple sclerosis, diabetes mellitus, inflammatory bowel  
CC disease and Crohn's disease. The antibodies can also be used for treating  
CC immunologic renal diseases, glomerulonephritis, mesangiolipidiferative  
CC disease, chronic lymphocytic leukaemia, secondary glomerulonephritis or  
CC vasculitis associated with lupus, polyarteritis, scleroderma, HIV-related  
CC diseases, amyloidosis and haemolytic uraemic syndrome. (I) and the  
CC antibodies can also be used for renal or urological neoplasms and  
CC multiple myelomas, asthma, bronchitis, emphysema and other chronic airway  
CC diseases. Human zcytor19 is located to chromosome 1, more specifically to  
CC chromosome 1p36.11. The present sequence represents a human IgG gamma 1  
CC heavy chain protein, which is used in an example from the present  
CC invention

SQ Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 5; Length 330;  
Best Local Similarity 97.9%; Pred. No. 1.8e-122;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKPSVPLPSSKSTSGTAAAGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
DB 1 ASTKPSVPLPSSKSTSGTAAAGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
QY 61 GLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHPCPCPAPELLGG 120  
DB 61 GLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHPCPCPAPELLGG 120  
QY 121 PSVFLPPEPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVVHNNAKTRPEEQYN 180  
DB 121 PSVFLPPEPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVVHNNAKTRPEEQYN 180  
QY 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240  
DB 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240  
QY 241 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300  
DB 241 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300  
QY 301 QOQNVFSCSVMHGALHNHYTQKSLSLSPGK 330  
DB 301 QOQNVFSCSVMHGALHNHYTQKSLSLSPGK 330

RESULT 6  
ABB05736  
ID ABB05736 standard; protein; 330 AA.

AC ABB05736;

XX

DT 01-MAY-2002 (first entry)

DE Human immunoglobulin G gamma 1 protein sequence SEQ ID NO:38.

XX Zcytor17; chromosome 5; Sg11; cytokine receptor; immunomodulatory;  
XX antirheumatic; antiarthritic; neuroprotective; anti-inflammatory;  
XX muscular; lymphoid; immune; inflammatory; splenic; blood; bone;

infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease; autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer; inflammatory disease; pancreatitis; inflammatory bowel disease.

Homo sapiens.

WO200200721-A2.

03-JAN-2002.

26-JUN-2001; 2001WO-US020484.

26-JUN-2000; 2000US-0214282P.

29-JUN-2000; 2000US-0214955P.

08-FEB-2001; 2001US-0267963P.

(ZYMO) ZYMOGENETICS INC.

Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL, Maurer MF;

WPI; 2002-090519/12.

N-PSDB; ABA93797.

Isolated polynucleotide encoding a cytokine receptor zcytor17 which is useful for treating and diagnosing lymphoid, immune, inflammatory, splenic, blood or bone disorders.

Example 17; Page 187-188; 235pp; English.

The present invention describes a cytokine receptor designated zcytor17. Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic, antirheumatic, antiarthritic and muscular activities. The zcytor17 proteins are useful for treating and diagnosing lymphoid, immune, inflammatory, splenic, blood or bone disorders. Agonists or anti-zcytor17 antibodies are useful in stimulating cell-mediated immunity and for stimulating lymphocyte proliferation, such as in the treatment of infections involving immunosuppression, including certain viral infections. They are also useful for inducing cytotoxicity and for treating leukopenias. Antagonist of zcytor17 polypeptides are useful for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer, pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to ABA93843 and ABB05730 to ABB05745 represent sequences used in the exemplification of the present invention

Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 5; Length 330;  
Best Local Similarity 97.9%; Pred. No. 1.8e-122;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 ASTGSPVPLABSSKSTSGTAAAGCLVNDYPPPEPVTSWNSGALTSVHTPPAVLQSS 60  
1 ASTKGSVPPLABSSKSTSGTAAAGCLVNDYPPPEPVTSWNSGALTSVHTPPAVLQSS 60

61 GLYSLSVVTVBSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKHTCTPCPCAPBLGG 120  
61 GLYSLSVVTVBSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKHTCTPCPCAPBLGG 120

121 PSVFLPFPKPKDTLMTSRTPETVCVVVDVSHEDPEVFNMYVGVGEVHNKTKPREBOYN 180  
121 PSVFLPFPKPKDTLMTSRTPETVCVVVDVSHEDPEVFNMYVGVGEVHNKTKPREBOYN 180

181 STYRVSVTLTVLHQNMMNGEKYCKVSNKALPAPIEKTISKAVQPREPOVYTLPPSRDE 240  
181 STYRVSVTLTVLHQNMMNGEKYCKVSNKALPAPIEKTISKAVQPREPOVYTLPPSRDE 240

241 LTNQVSLTCLVAGFYPDSIDAVWESNGQPENNYKTPPVLDSVGSFYLYSKLTVDKSRW 300  
241 LTNQVSLTCLVAGFYPDSIDAVWESNGQPENNYKTPPVLDSVGSFYLYSKLTVDKSRW 300

301 OQGNVFGCVMEBALNHYQORSLSLSPCK 330  
301 OQGNVFGCVMEBALNHYQORSLSLSPCK 330

RESULT 7  
ID ABP71856 standard; protein; 330 AA.  
AC ABP71856;  
DT 17-APR-2003 (first entry)  
DE Human IgG1 Fcgamma region.  
KW Human; fusion protein; IGE Fcpepsilon; Igg Fcgamma; FcpepsilonRI; allergy; allergic asthma; FcgammaRIIB; protein therapy; IGE; Igg; asthma; hay fever; atopic dermatitis; drug allergy; peanut allergen.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Region 1..98  
FT Region /label= CH1 region  
FT Region 99..113  
FT Region /label= Hinge\_region  
FT Region 114..223  
FT Region /label= CH2\_region  
FT Region 224..330  
FT Region /label= CH3\_region  
PN WO2002102320-A2.  
PD 27-DEC-2002.  
PF 14-JUN-2002; 2002WO-US019448.  
PR 15-JUN-2001; 2001US-0298710P.  
PA (TANCO-) TANCOX INC.  
PI An L, Wu H, Fung MSC;  
DR WPI; 2003-167440/16.  
PT New fusion protein which binds to FcpepsilonRI or RIi receptor and FcgammaRIIB receptor, useful for treating or preventing allergies and asthma, comprises an IGE Fcpepsilon fragment and an Igg Fcgamma fragment.  
PS Disclosure; Fig 5; 32pp; English.  
XX The invention relates to a novel fusion protein comprising an Igg Fcpepsilon fragment and an Igg Fcgamma fragment, which binds to an FcpepsilonRI and/or FcpepsilonRIi receptor and an FcgammaRIIB receptor. The fusion protein of the invention may have a use in protein therapy. The fusion protein is useful in treating or preventing IGE-mediated allergies and asthma, such as allergic asthma, allergic rhinitis, hay fever, food allergy, atopic dermatitis and drug allergy. The allergic response is particularly caused by peanut allergen. The present sequence represents the human IgG1 Fcgamma fragment

Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 6; Length 330;  
Best Local Similarity 97.9%; Pred. No. 1.8e-122;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 ASTGSPVPLABSSKSTSGTAAAGCLVNDYPPPEPVTSWNSGALTSVHTPPAVLQSS 60  
1 ASTKGSVPPLABSSKSTSGTAAAGCLVNDYPPPEPVTSWNSGALTSVHTPPAVLQSS 60

61 GLYSLSVVTVBSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKHTCTPCPCAPBLGG 120

DB 61 GLYSLSVTVTVSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPAPABELLG 120  
QY 121 PSVFLPPEPKDGLMISRTPEVTCVVDVSHEDPEVKFNMYDGVENVNKTTPREEQYN 180  
DB 121 PSVFLPPEPKDGLMISRTPEVTCVVDVSHEDPEVKFNMYDGVENVNKTTPREEQYN 180  
QY 181 STYRVAVSVLTVLHQMNGKEYKCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDE 240  
DB 181 STYRVAVSVLTVLHQMNGKEYKCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDE 240  
QY 241 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRM 300  
DB 241 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRM 300  
QY 301 QQGNVFSQSVMEALHNHYOQRSLSLSPGK 330  
DB 301 QQGNVFSQSVMEALHNHYOQRSLSLSPGK 330

## RESULT 8

AAE32915  
ID AAE32915 standard; protein; 330 AA.

AC AAE32915;

DT 24-MAR-2003 (first entry)

DE Human immunoglobulin G1 (IgG1) heavy chain Fc region.

KW T-cell; immunogenic; therapy; human; immunoglobulin G1; IgG1.

OS Homo sapiens.

PN WO200279232-A2.

PD 10-OCT-2002.

PF 30-MAR-2002; 2002WO-US009815.

PR 30-MAR-2001; 2001US-0280625P.

PA (LEXI-) LEXIGEN PHARM CORP.

PI Gillette SD;

DR WPI; 2003-103259/09.

PT Reducing the immunogenicity of a fusion protein comprises changing an amino acid within the junction region to reduce the ability of the candidate T-cell epitope identified within the junction spanning to interact with T-cell receptor.

PS Disclosure; Page 49-50; 68pp; English.

CC The invention relates to a method for reducing the immunogenicity of a fusion protein which involves identifying a candidate T-cell epitope within a junction spanning a fusion junction of a fusion protein, and changing an amino acid within the junction region to reduce the ability of the candidate T-cell epitope to interact with a T-cell receptor. The method is useful for reducing the immunogenicity of a fusion protein. It is useful for analyzing, changing or modifying one or more amino acids in the junction region of a fusion protein to identify a T-cell epitope and reduce its ability to interact with a T-cell receptor. The less immunogenic fusion proteins are useful in providing therapeutic treatment. The present sequence is human immunoglobulin G1 (IgG1) heavy chain Fc region used to illustrate the method of the invention

XX Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 6; Length 330;  
Best Local Similarity 97.9%; Pred. No. 1,8e-122;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKPSVPEPLAPSSKSTSGTAALGCLVKDYFPEPVTVSNMNSGALTSGVHPFPAVLQSS 60  
DB 1 ASTKPSVPEPLAPSSKSTSGTAALGCLVKDYFPEPVTVSNMNSGALTSGVHPFPAVLQSS 60  
QY 61 GLYSLSVTVTVSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPAPABELLG 120  
DB 61 GLYSLSVTVTVSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPAPABELLG 120  
QY 121 PSVFLPPEPKDGLMISRTPEVTCVVDVSHEDPEVKFNMYDGVENVNKTTPREEQYN 180  
DB 121 PSVFLPPEPKDGLMISRTPEVTCVVDVSHEDPEVKFNMYDGVENVNKTTPREEQYN 180  
QY 181 STYRVAVSVLTVLHQMNGKEYKCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDE 240  
DB 181 STYRVAVSVLTVLHQMNGKEYKCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDE 240  
QY 241 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRM 300  
DB 241 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRM 300  
QY 301 QQGNVFSQSVMEALHNHYOQRSLSLSPGK 330  
DB 301 QQGNVFSQSVMEALHNHYOQRSLSLSPGK 330

## RESULT 9

AAE32627  
ID AAE32627 standard; protein; 330 AA.

AC AAE32627;

DT 24-MAR-2003 (first entry)

DE Human immunoglobulin G1 (IgG1) heavy chain Fc region.

KW Human; immunogenic; therapy; immunoglobulin G1; IgG1.

OS Homo sapiens.

PN WO200279415-A2.

PD 10-OCT-2002.

PF 29-MAR-2002; 2002WO-US009650.

PR 30-MAR-2001; 2001US-0280625P.

PA (LEXI-) LEXIGEN PHARM CORP.

PI Gillette SD;

DR WPI; 2003-111794/10.

PT Reducing the immunogenicity of a fusion protein by changing an amino acid within the junction region spanning a fusion junction of a fusion protein to reduce the ability of the candidate T-cell epitope to interact with a T-cell receptor.

PS Disclosure; Page 49-50; 67pp; English.

CC The present invention relates to a method of reducing the immunogenicity of a fusion protein. The method involves identifying a candidate T-cell epitope within a junction region spanning a fusion junction of a fusion protein and changing an amino acid within the junction region to reduce the ability of the candidate T-cell epitope to interact with a T-cell receptor. The method is useful for reducing the immunogenicity of fusion proteins for use in therapy. The present sequence is human immunoglobulin G1 (IgG1) heavy chain Fc region. This sequence is used to illustrate the method of the invention

XX Sequence 330 AA;

Query Match	98.0%	Score 1729;	DB 6;	Length 330;
Best Local Similarity	97.9%;	Pred. No. 1.8e-122;		
Matches 323;	Conservative 3;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	1	ASTGKPSFPLAPSSKSTSGGTAALGCLVKDYFPEPVWMTNMSGALTSGVTHFPAVLGG	60	
Db	1	ASTGKPSFPLAPSSKSTSGGTAALGCLVKDYFPEPVWMTNMSGALTSGVTHFPAVLGG	60	
Qy	61	GLYSLSVVTVPSSSLGTQYICNVNHRKPSNTKVKKEPKSCDTHHTCPCPABELLGG	120	
Db	61	GLYSLSVVTVPSSSLGTQYICNVNHRKPSNTKVKKEPKSCDTHHTCPCPABELLGG	120	
Qy	121	PSVFLFPKPKPDOTLMTISRPETCVVVDVSHDEPEVKFNWYDGYVHNVKTPEBOYN	180	
Db	121	PSVFLFPKPKPDOTLMTISRPETCVVVDVSHDEPEVKFNWYDGYVHNVKTPEBOYN	180	
Qy	181	STYVWSVLTVLHOMWNGKEKCVSKNALPAPLEKITSKAKVQPREBOVYTLPPSRDE	240	
Db	181	STYVWSVLTVLHOMWNGKEKCVSKNALPAPLEKITSKAKVQPREBOVYTLPPSRDE	240	
Qy	241	LTKQVSLTCLVKGFPSPDIWEMESNGQPENNYKTPPEVLDSVGSFPLYSKLTVDKSRW	300	
Db	241	LTKQVSLTCLVKGFPSPDIWEMESNGQPENNYKTPPEVLDSVGSFPLYSKLTVDKSRW	300	
Qy	301	QOGNVFSCSVMEALHNHYQORSLSPGK 330		
Db	301	QOGNVFSCSVMEALHNHYQORSLSPGK 330		
RESULT 10				
ID	ABR82103	standard; protein; 330 AA.		
XX	ABR82103;			
AC	ABR82103;			
XX	23-SEP-2003	(first entry)		
DT	23-SEP-2003	(first entry)		
DE	Human DR6 related amino acid sequence SEQ ID NO:5.			
XX	Human DR6 related amino acid sequence SEQ ID NO:5.			
KM	Human; DR6; B-cell mediated disease; immunosuppressive; antirheumatic;			
KM	antiarthritic; antistaphylococcal; dermatological; antiinflammatory;			
KM	antiparasitic; antidiabetic; cytostatic; neuroprotective; thyromimetic;			
KM	antichyroid; nephrotropic; antileptile; vasotrophic; vitaminic;			
KM	hepatocytotropic; antibacterial; antitumor; haemostatic; antianemic;			
KM	antimicrobial; anti-HIV; DR6 agonist; DR6 antagonist; immunity.			
XX	Homo sapiens.			
OS	Homo sapiens.			
XX	WO2003051290-A2.			
PN	26-JUN-2003.			
PD	26-JUN-2003.			
XX	10-DEC-2002; 2002WO-US037596.			
PF	10-DEC-2002; 2002WO-US037596.			
XX	17-DEC-2001; 2001US-0342632P.			
PR	17-DEC-2001; 2001US-0342632P.			
XX	(ELIL ) LILLY & CO ELI.			
PA	(ELIL ) LILLY & CO ELI.			
XX	Liu J, Na S, Song HY, Yang D;			
PI	Liu J, Na S, Song HY, Yang D;			
XX	WPI; 2003-541604/51.			
DR	WPI; 2003-541604/51.			
XX	Treating or preventing a B cell mediated condition e.g., chronic			
PT	hepatitis or chronic cirrhosis, in a mammal by administering a			
PT	pharmaceutical composition comprising a DR6 agonist or DR6 antagonist to			
PT	the mammal.			
XX	Disclosure; Page 96-97; 97pp; English.			
PS	The present invention describes a method (M1) for treating or preventing			
CC	a B cell mediated condition in a mammal by administering a pharmaceutical			
CC	composition comprising a DR6 agonist or DR6 antagonist to the mammal.			
CC	Also described: (1) inhibiting B cell mediated immunity in a mammal, by			

Query Match	98.0%	Score 1729	DB 6	Length 330
Best Local Similarity	97.9%	Pred. No. 1.8e-122		
Matches 323	Conservative 3	Mismatches 4	Indels 0	Gaps 0
QY	1	ASTGPGSYFLPABSSKSTSGTALGCLVNDYFPPEPTVMNGALNSGVHTPAVYLOSS	60	
Db	1	ASTGPGSYFLPABSSKSTSGTALGCLVNDYFPPEPTVMNSGALNSGVHTPAVYLOSS	60	
QY	61	GLYSLSVVVYVWSSSLGTQYICNVNHNKPSNTKDKVKEPSCKYTCPCPPELILGG	120	
Db	61	GLYSLSVVVYVWSSSLGTQYICNVNHNKPSNTKDKVKEPSCKYTCPCPPELILGG	120	
QY	121	PSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDDEVKFNMYVDGVEVHNVKTKPREQYN	180	
Db	121	PSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDDEVKFNMYVDGVEVHNVKTKPREQYN	180	
QY	181	STRVSVSLVTLTHQDMNNGKRYKCKVNSKNKLPALIEKTTISAKAKYQPREPOVYTLPSERDE	240	
Db	181	STRVSVSLVTLTHQDMNNGKRYKCKVNSKNKLPALIEKTTISAKAKYQPREPOVYTLPSERDE	240	
QY	241	LTKNQVSLTCLVKGFYPSDIAVEENSGKQPENNYKTPPVLDSDGVSGFSLYSKLTVDLSRW	300	
Db	241	LTKNQVSLTCLVKGFYPSDIAVEENSGKQPENNYKTPPVLDSDGVSGFSLYSKLTVDLSRW	300	
QY	301	QQGNVFCGVNHEALHNHYQOQSLSISPGK	330	
Db	301	QQGNVFCGVNHEALHNHYQOQSLSISPGK	330	

RESULT 11

AA031102

ID AA031102 standard; protein; 330 AA.  
XX  
AC AA031102;  
XX  
DT 06-OCT-2003 (first entry)  
XX  
DE Human A2-G8 SCF antibody heavy chain constant region.  
XX  
KW Human; antibody; stem cell factor; mast cell growth factor; asthma; SCF;  
KM steel factor; c-kit ligand; gene therapy; heavy chain.  
XX  
OS Homo sapiens.  
XX  
PN WO2003051311-A2.  
XX  
PD 26-JUN-2003.  
XX  
PF 16-DEC-2002; 2002WO-US040227.  
XX  
PR 17-DEC-2001; 2001US-0342174P.  
XX  
PA (FARB ) BAYER CORP.  
XX  
PI Takeuchi T, Tomkinson A, Neben S;  
XX  
DR WPI; 2003-523500/49.  
XX  
DR N-PSDB; AAL62618.  
XX  
PT New purified human antibody that binds to stem cell factor protein,  
XX  
PT useful for preparing a composition for treating asthma.  
XX  
PS Example 10; Page 47-48; 94pp; English.  
XX  
PS The invention provides human antibodies that bind to stem cell factor  
CC (SCF) protein. SCF is also known as mast cell growth factor, steel factor  
CC or c-kit ligand. Antibodies of the invention are useful for preparing  
CC compositions for treating asthma. They are also used in gene therapy. The  
CC present sequence is human SCF antibody heavy chain constant region  
XX  
SQ Sequence 330 AA;  
XX  
Query Match 98.0%; Score 1729; DB 6; Length 330;  
Best Local Similarity 97.9%; Pred. No. 1.8e-122;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
XX  
QY 1 ASTKGPSVPLAPSSKSTSGGTALGCLVKDYFPEPEVTVSNMSGALTSGVHFPVAVLQSS 60  
1 ASTKGPSVPLAPSSKSTSGGTALGCLVKDYFPEPEVTVSNMSGALTSGVHFPVAVLQSS 60  
DB 61 GLYSLSVVTVPSSSLSIGTQTYICNVNHRKPSNTKVDKKVEPKSCDKTHTCPCPAPPELLGG 120  
61 GLYSLSVVTVPSSSLSIGTQTYICNVNHRKPSNTKVDKKVEPKSCDKTHTCPCPAPPELLGG 120  
QY 121 PSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVVHNAKTKRPREQYN 180  
121 PSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVVHNAKTKRPREQYN 180  
DB 121 PSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVVHNAKTKRPREQYN 180  
121 PSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVVHNAKTKRPREQYN 180  
QY 181 STYRVVSVTLTVLHQMNGKEKCYKNKALPAPIEKITSKAKVQPREQVYTLPPSRDE 240  
181 STYRVVSVTLTVLHQMNGKEKCYKNKALPAPIEKITSKAKVQPREQVYTLPPSRDE 240  
DB 181 STYRVVSVTLTVLHQMNGKEKCYKNKALPAPIEKITSKAKVQPREQVYTLPPSRDE 240  
181 STYRVVSVTLTVLHQMNGKEKCYKNKALPAPIEKITSKAKVQPREQVYTLPPSRDE 240  
QY 241 LTRKQVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDSGSEFLYSKLTVDKSRW 300  
241 LTRKQVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDSGSEFLYSKLTVDKSRW 300  
DB 241 LTRKQVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDSGSEFLYSKLTVDKSRW 300  
241 LTRKQVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDSGSEFLYSKLTVDKSRW 300  
QY 301 QOGNVFSCSVMEHALHNHYQQRSLSPK 330  
301 QOGNVFSCSVMEHALHNHYQQRSLSPK 330  
DB 301 QOGNVFSCSVMEHALHNHYQQRSLSPK 330  
301 QOGNVFSCSVMEHALHNHYQQRSLSPK 330  
RESULT 12  
ABR55836  
1P ABR55836 standard; proteoin; 330 AA.

XX  
AC ABR55836;  
XX  
DT 02-SEP-2003 (first entry)  
XX  
DE Anti-Ang-2 antibody IgG1 constant region.  
XX  
KW Ang-2; angiotensin-2; anorectic; cyrostatic; antiarteriosclerotic;  
KM gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;  
KW angiogenesis; antibody; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2003030833-A2.  
XX  
PD 17-APR-2003.  
XX  
PF 11-OCT-2002; 2002WO-US032613.  
XX  
PR 11-OCT-2001; 2001US-0328604P.  
XX  
PR 10-OCT-2002; 2002US-00269805.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Oliner JD;  
XX  
DR WPI; 2003-504963/47.  
XX  
DR New specific binding agents (i.e. anti-Angiotensin-2 antibodies), useful  
XX  
PT for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,  
XX  
PT hemangioma, arteriosclerosis, atherosclerosis or endometriosis.  
XX  
PS Example 4; Page 96; 161pp; English.  
XX  
PS The invention relates to a specific binding agent, which comprises at  
CC least one peptide selected from any of 62 peptides (ABR55769-830) or its  
CC fragment. The binding agents are antibodies that recognize and bind to  
CC angiotensin-2 (Ang-2). The specific binding agent, particularly the  
CC antibody, is useful for inhibiting undesired angiogenesis, treating  
CC cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-  
CC 2 activity, modulating vascular permeability or plasma leakage, or  
CC treating a disease (e.g. ocular neovascular disease, obesity,  
CC haemangioma, haemangioma, arteriosclerosis, inflammatory disease,  
CC inflammatory disorders, atherosclerosis, endometriosis, neoplastic  
CC disease, bone-related disease, or psoriasis) in a mammal. The present  
CC sequence represents a human IgG1 constant region of an anti-Ang-2  
XX  
SQ Sequence 330 AA;  
XX  
Query Match 98.0%; Score 1729; DB 6; Length 330;  
Best Local Similarity 97.9%; Pred. No. 1.8e-122;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
XX  
QY 1 ASTKGPSVPLAPSSKSTSGGTALGCLVKDYFPEPEVTVSNMSGALTSGVHFPVAVLQSS 60  
1 ASTKGPSVPLAPSSKSTSGGTALGCLVKDYFPEPEVTVSNMSGALTSGVHFPVAVLQSS 60  
DB 61 GLYSLSVVTVPSSSLSIGTQTYICNVNHRKPSNTKVDKKVEPKSCDKTHTCPCPAPPELLGG 120  
61 GLYSLSVVTVPSSSLSIGTQTYICNVNHRKPSNTKVDKKVEPKSCDKTHTCPCPAPPELLGG 120  
QY 121 PSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVVHNAKTKRPREQYN 180  
121 PSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVVHNAKTKRPREQYN 180  
DB 121 PSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVVHNAKTKRPREQYN 180  
121 PSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVVHNAKTKRPREQYN 180  
QY 181 STYRVVSVTLTVLHQMNGKEKCYKNKALPAPIEKITSKAKVQPREQVYTLPPSRDE 240  
181 STYRVVSVTLTVLHQMNGKEKCYKNKALPAPIEKITSKAKVQPREQVYTLPPSRDE 240  
DB 181 STYRVVSVTLTVLHQMNGKEKCYKNKALPAPIEKITSKAKVQPREQVYTLPPSRDE 240  
181 STYRVVSVTLTVLHQMNGKEKCYKNKALPAPIEKITSKAKVQPREQVYTLPPSRDE 240  
QY 241 LTRKQVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDSGSEFLYSKLTVDKSRW 300  
241 LTRKQVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDSGSEFLYSKLTVDKSRW 300  
DB 241 LTRKQVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDSGSEFLYSKLTVDKSRW 300  
241 LTRKQVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDSGSEFLYSKLTVDKSRW 300

QY 301 OQGNVFGSCVMHEALHNHYQOQSLSLSPGK 330  
 DB 301 OQGNVFGSCVMHEALHNHYTOKSLSLSPGK 330

## RESULT 13

AAO30893  
 ID AAO30893 standard; protein; 330 AA.

AAO30893;  
 AC AAO30893;  
 XX  
 XX

DT 22-SEP-2003 (first entry)  
 XX

DE Human immunoglobulin gamma (IgG) 1 constant region.  
 XX

XX Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;  
 XX gene therapy; immunoglobulin; Ig; human.  
 XX

OS Homo sapiens.  
 XX

PN WO2003048334-A2.  
 XX

PD 12-JUN-2003.  
 XX

PF 04-DEC-2002; 2002WO-US038780.  
 XX

PR 04-DEC-2001; 2001US-037113P.  
 XX

PR 12-APR-2002; 2002US-0371966P.  
 XX

PA (EMDL-) EMD LEXIGEN RES CENT CORP.  
 XX

PI Gililies SD;  
 XX

DR WPI: 2003-513757/48.  
 XX

PT New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2  
 PT moiety, useful for preparing a composition for treating cancer, viral  
 PT infections or immune disorders.  
 XX

PS Example 1; Page 51-53; 71pp; English.  
 XX

CC The invention relates to cytokine fusion proteins with increased  
 CC therapeutic index and methods for increasing the therapeutic index of  
 CC such fusion proteins. The fusion protein comprises a non-interleukin-2  
 CC (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a  
 CC composition for treating cancer, viral infections or immune disorders.  
 CC The fusion protein is also used in gene therapy. The present sequence is  
 CC human immunoglobulin gamma (IgG) constant region. This sequence is used  
 CC to illustrate the method of the invention  
 XX

SO Sequence 330 AA;  
 XX

Query Match 98.0%; Score 1729; DB 6; Length 330;  
 Best Local Similarity 97.9%; Pred. No. 1.8e-122;

Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKPSVPLPSSKSTSGTAAAGCLVKDYFPEPVYTVSNMGSALTSGVHTFPAVLQSS 60  
 DB 1 ASTKPSVPLPSSKSTSGTAAAGCLVKDYFPEPVYTVSNMGSALTSGVHTFPAVLQSS 60

QY 61 GLYSLSVTVTVSSSLGTQTYICNVNHNKPSNTRKVDKVPKSCDKHTTCTPCPAPRLGG 120  
 DB 61 GLYSLSVTVTVSSSLGTQTYICNVNHNKPSNTRKVDKVPKSCDKHTTCTPCPAPRLGG 120

QY 121 PSVPLPPEPKDITLMISRTPEVTCVVVDVSHEDPEVKFMWYVDGVEVHNAVTKPRREQYN 180  
 DB 121 PSVPLPPEPKDITLMISRTPEVTCVVVDVSHEDPEVKFMWYVDGVEVHNAVTKPRREQYN 180

QY 181 STYRVAVSLTVLHOMNMNGEYKCKVSNKALPAPIEKTISKAKVQPREQVYTLPPSRDE 240  
 DB 181 STYRVAVSLTVLHOMNMNGEYKCKVSNKALPAPIEKTISKAKVQPREQVYTLPPSRDE 240

QY 241 LTRNOVSLTCLVKGFPSPDIAVWESNGOPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW 300  
 DB 241 LTRNOVSLTCLVKGFPSPDIAVWESNGOPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW 300

QY 301 OQGNVFGSCVMHEALHNHYQOQSLSLSPGK 330  
 DB 301 OQGNVFGSCVMHEALHNHYTOKSLSLSPGK 330

## RESULT 14

ADFL1389  
 ID ADFL1389 standard; protein; 330 AA.

ADFL1389;  
 AC ADFL1389;  
 XX  
 XX

DT 12-FEB-2004 (first entry)  
 XX

DE Anti-OPGL antibody heavy chain constant region SEQ ID NO:2.  
 XX

XX human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;  
 XX osteopathic; antiarthritis; cycostatic; gene therapy; bone disorder;  
 XX osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.  
 XX

OS Homo sapiens.  
 XX

PN WO2003086289-A2.  
 XX

PD 23-OCT-2003.  
 XX

PF 07-APR-2003; 2003WO-US010749.  
 XX

PR 05-APR-2002; 2002US-0370407P.  
 XX

PA (AMGE-) AMGEN INC.  
 XX

PI Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;  
 XX

DR WPI: 2003-845253/78.  
 XX

DR N-PSDB; ADFL1388.  
 XX

PT New isolated antibody that specifically binds osteoprotegerin ligand,  
 PT useful for diagnosing or treating bone disorders, such as osteoporosis,  
 PT bone loss from arthritis, Paget's disease or osteopenia.  
 XX

PS Example 3; SEQ ID NO 2; 156pp; English.  
 XX

CC The present invention describes an isolated human antibody (1) that  
 CC specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a  
 CC pharmaceutical composition comprising a pharmaceutical carrier and a  
 CC therapeutic amount of (1); (2) methods of treating an osteopenic disorder  
 CC in a patient, comprising administering to a patient the pharmaceutical  
 CC composition of (1) or a pharmaceutical amount of (1); and (3) a method  
 CC for detecting OPGL in a biological sample, comprising contacting the  
 CC sample with (1) under conditions that allow for binding of the antibody  
 CC to OPGL, and measuring the level of bound antibody in the sample. (1) has  
 CC osteopathic, antiarthritis and cycostatic activities, and can be used in  
 CC gene therapy. The composition and methods are useful in diagnosing or  
 CC treating bone disorders, such as osteoporosis, bone loss from arthritis,  
 CC Paget's disease or osteopenia. The antibody (1) may also be used for  
 CC detecting OPGL in biological samples and in identifying cells or tissues  
 CC that produce the protein. The present sequence represents a sequence  
 CC which is used in the exemplification of the present invention.  
 XX

SO Sequence 330 AA;  
 XX

Query Match 98.0%; Score 1729; DB 7; Length 330;  
 Best Local Similarity 97.9%; Pred. No. 1.8e-122;

Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKPSVPLPSSKSTSGTAAAGCLVKDYFPEPVYTVSNMGSALTSGVHTFPAVLQSS 60  
 DB 1 ASTKPSVPLPSSKSTSGTAAAGCLVKDYFPEPVYTVSNMGSALTSGVHTFPAVLQSS 60

QY 61 GLYSLSVVTVPSSSLGQTOTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPCPAPPELLGG 120  
DB 61 GLYSLSVVTVPSSSLGQTOTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPCPAPPELLGG 120  
QY 121 PSVFLEPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFMVYDGYEVHNVKTKPREEOYN 180  
DB 121 PSVFLEPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFMVYDGYEVHNVKTKPREEOYN 180  
QY 181 STYRVVSVLTVLHQMNGKEYCKVSNKALPAPIEKTISKAKVQPREQVYTLPPSRDE 240  
DB 181 STYRVVSVLTVLHQMNGKEYCKVSNKALPAPIEKTISKAKVQPREQVYTLPPSRDE 240  
QY 241 LTKNOVSLTCLVKGYPSPDIAVEMESNGQPENNYKTTTPVLDVSFGFVLSKLTVDKSRW 300  
DB 241 LTKNOVSLTCLVKGYPSPDIAVEMESNGQPENNYKTTTPVLDVSFGFVLSKLTVDKSRW 300  
QY 301 QOGNVFSCSVNHEALHNHYQKRSLSLSPGK 330  
DB 301 QOGNVFSCSVNHEALHNHYQKRSLSLSPGK 330

## RESULT 15

ADE97351  
ID ADE97351 standard; protein; 330 AA.

AC ADE97351;

DT 12-FEB-2004 (first entry)

DE Human IgG1 heavy chain constant region protein - SEQ ID 20.

XX immunoadhesin; immunoglobulin heavy chain; J chain; joining; toxin;  
KW virucide; antibacterial; anthrax; rhinovirus infection; common cold;  
KW intercellular adhesion molecule; ICAM-1; human; constant region; IgG.

OS Homo sapiens.

PN WO2003064992-A2.

PD 07-AUG-2003.

PE 25-OCT-2002; 2002MO-US034197.

PR 26-OCT-2001; 2001US-00047542.

PA (PLAN-) PLANET BIOTECHNOLOGY INC.

PA (LARR/) LARRICK J W.

PA (WYCO/) WYCOFF K L.

PI Larrick JW, Wycoff KL;

DR WPI; 2003-636816/60.

DR N-PSDB; ADE97350, ADE97376.

PT New immunoadhesin, useful for treating anthrax and rhinovirus, comprises  
PT chimeric toxin receptor protein linked to immunoglobulin heavy chain, and  
PT J chain and secretory component associated with the chimeric toxin  
PT receptor protein.

PS Disclosure; SEQ ID NO 20; 288bp; English.

XX The invention relates to a novel immunoadhesin comprising a chimeric  
CC toxin receptor protein consisting of a toxin receptor protein linked to  
CC at least a portion of an immunoglobulin heavy chain with a J (joining)  
CC chain and secretory component (SC) associated with the chimeric toxin  
CC receptor protein. The immunoadhesin comprises a chimeric bacterial or  
CC viral toxin receptor protein and the immunoadhesin has plant-specific  
CC glycosylation. The immunoadhesin of the invention demonstrates virucide  
CC and antibacterial activities and may be useful for reducing the binding  
CC of a viral or bacterial antigen to a host cell and thus for treating or  
CC preventing anthrax, as well as human rhinovirus infection which results  
CC in the common cold. The current sequence is that of the human  
CC immunoadhesin-related protein of the invention.

XX  
SQ Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 7; Length 330;  
Best Local Similarity 97.9%; Pred. No. 1.8e-122;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSPVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNSGALTSGVHTFPAVLQSS 60  
DB 1 ASTKGPSPVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNSGALTSGVHTFPAVLQSS 60  
QY 61 GLYSLSVVTVPSSSLGQTOTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPCPAPPELLGG 120  
DB 61 GLYSLSVVTVPSSSLGQTOTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPCPAPPELLGG 120  
QY 121 PSVFLEPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFMVYDGYEVHNVKTKPREEOYN 180  
DB 121 PSVFLEPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFMVYDGYEVHNVKTKPREEOYN 180  
QY 181 STYRVVSVLTVLHQMNGKEYCKVSNKALPAPIEKTISKAKVQPREQVYTLPPSRDE 240  
DB 181 STYRVVSVLTVLHQMNGKEYCKVSNKALPAPIEKTISKAKVQPREQVYTLPPSRDE 240  
QY 241 LTKNOVSLTCLVKGYPSPDIAVEMESNGQPENNYKTTTPVLDVSFGFVLSKLTVDKSRW 300  
DB 241 LTKNOVSLTCLVKGYPSPDIAVEMESNGQPENNYKTTTPVLDVSFGFVLSKLTVDKSRW 300  
QY 301 QOGNVFSCSVNHEALHNHYQKRSLSLSPGK 330  
DB 301 QOGNVFSCSVNHEALHNHYQKRSLSLSPGK 330

Search completed: June 7, 2005, 08:56:37  
Job time : 172.565 secs



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OM protein - protein search, using sw model

Run on: June 7, 2005, 09:01:44 ; Search time 144.767 Seconds

(without alignments)  
821.093 Million cell updates/sec

Title: US-10-000-439-2

Perfect score: 1764

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599520 seqs, 360203123 residues

Total number of hits satisfying chosen parameters: 1599520

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1764	100.0	330	10	US-10-000-439-2
3	1729	98.0	330	10	US-09-995-898A-15
4	1729	98.0	330	10	US-09-892-949-38
5	1729	98.0	330	13	US-10-047-542-20
6	1729	98.0	330	14	US-10-269-805-68
7	1729	98.0	330	14	US-10-310-719-8
8	1729	98.0	330	14	US-10-112-583-1
9	1729	98.0	330	14	US-10-320-231A-81
10	1729	98.0	330	15	US-10-383-902A-6
11	1729	98.0	330	15	US-10-408-901-2
12	1729	98.0	330	15	US-10-420-034A-15

13	1729	98.0	330	15	US-10-257-907-5	Sequence 5, Appli
14	1729	98.0	330	15	US-10-656-769-2	Sequence 2, Appli
15	1729	98.0	330	16	US-10-772-531-38	Sequence 38, Appli
16	1729	98.0	330	16	US-10-479-326-1	Sequence 1, Appli
17	1729	98.0	330	16	US-10-815-449-8	Sequence 8, Appli
18	1729	98.0	332	10	US-09-990-586-98	Sequence 98, Appli
19	1729	98.0	332	14	US-10-310-113-167	Sequence 167, App
20	1729	98.0	332	14	US-10-230-880-98	Sequence 98, Appli
21	1729	98.0	333	15	US-10-272-899A-8	Sequence 8, Appli
22	1729	98.0	356	15	US-10-272-899A-72	Sequence 72, Appli
23	1729	98.0	371	14	US-10-157-408-7	Sequence 7, Appli
24	1729	98.0	371	14	US-10-097-044A-7	Sequence 7, Appli
25	1729	98.0	371	16	US-10-763-247-7	Sequence 7, Appli
26	1729	98.0	442	15	US-10-226-435A-12	Sequence 12, Appli
27	1729	98.0	442	15	US-10-487-322-12	Sequence 12, Appli
28	1729	98.0	442	16	US-10-487-326-12	Sequence 12, Appli
29	1729	98.0	442	16	US-10-487-326-21	Sequence 21, Appli
30	1729	98.0	442	16	US-10-486-908-12	Sequence 12, Appli
31	1729	98.0	442	16	US-10-486-908-16	Sequence 16, Appli
32	1729	98.0	444	14	US-10-150-475A-6	Sequence 6, Appli
33	1729	98.0	444	16	US-10-704-522-6	Sequence 6, Appli
34	1729	98.0	444	16	US-10-645-215-6	Sequence 6, Appli
35	1729	98.0	445	14	US-10-320-231A-79	Sequence 79, Appli
36	1729	98.0	445	15	US-10-408-901-34	Sequence 34, Appli
37	1729	98.0	445	15	US-10-408-901-42	Sequence 42, Appli
38	1729	98.0	445	15	US-10-408-901-30	Sequence 30, Appli
39	1729	98.0	446	15	US-10-408-901-38	Sequence 38, Appli
40	1729	98.0	446	15	US-10-408-901-46	Sequence 46, Appli
41	1729	98.0	446	15	US-10-408-901-50	Sequence 50, Appli
42	1729	98.0	446	15	US-10-435-229-7	Sequence 7, Appli
43	1729	98.0	447	10	US-09-256-156-1	Sequence 1, Appli
44	1729	98.0	448	15	US-10-378-567-2	Sequence 2, Appli
45	1729	98.0	449	16	US-10-635-908-16	Sequence 16, Appli

#### ALIGNMENTS

RESULT 1  
US-09-847-208-2  
; Publication US/09847208  
; File Name: US20030082190A1  
; GENERAL INFORMATION:  
; APPLICANT: Saxon, Andrew  
; APPLICANT: Zhang, Ke  
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF  
; TITLE OF INVENTION: IGB-MEDIATED ALLERGIC DISEASES  
; FILE REFERENCE: UC67.002A  
; CURRENT APPLICATION NUMBER: US/09/847,208  
; CURRENT FILING DATE: 2001-05-01  
; NUMBER OF SEQ ID NOS: 177  
; SOFTWARE: PatSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 330  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-847-208-2

Query Match	Score	1764	DB 10	Length	330
Best Local Similarity	100.0%	Pred. No. 1.1e-128			
Matches	330	Conservative	0	Mismatches	0
				Indels	0
				Gaps	0
QY	1	ASTKGPVFPPLAPSSKSTSGGTAAGCYKDYFPPEPVTVSMNSGALTSQVHFPAYLQSS	60		
DB	1	ASTKGPVFPPLAPSSKSTSGGTAAGCYKDYFPPEPVTVSMNSGALTSQVHFPAYLQSS	60		
QY	61	GLYSLSSVTVFSSLSGTQTYICNVHKKPSNTKVDKVAEPKSCDKHTKPCPAPRLGG	120		
DB	61	GLYSLSSVTVFSSLSGTQTYICNVHKKPSNTKVDKVAEPKSCDKHTKPCPAPRLGG	120		
QY	121	PSYFLFPKPKDTLMISRTPEVTVVVDVSHEDPEVKFMWYVDGVHNAVTKPREQYN	180		

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Db 121 PSVFLPPPKKDTLMISRPEVTCVVVDVSHEDPEVKFMWYDGVENHNVKTKRPREQYN 180
QY 181 STYRVVSVLTIVLHQMWMNGKEYCKVSNKALPAPIEKITSKAKVQPREQVYTLPPSRDE 240
Db 181 STYRVVSVLTIVLHQMWMNGKEYCKVSNKALPAPIEKITSKAKVQPREQVYTLPPSRDE 240
QY 241 LTRKNQVSLTCLVKGFPSPDIAVWESNNGOPENNYYKTPPVLDVSGSFFLYSKLTVDKSRW 300
Db 241 LTRKNQVSLTCLVKGFPSPDIAVWESNNGOPENNYYKTPPVLDVSGSFFLYSKLTVDKSRW 300
QY 301 OQGNVFSCSVMHGALHNHYQQRSLSLSPGK 330
Db 301 OQGNVFSCSVMHGALHNHYQQRSLSLSPGK 330

RESULT 2
US-10-000-439-2
; Sequence 2, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; TREATMENT OF IMMUNE DISEASES
; FILE REFERENCE: UC067,004A
; CURRENT APPLICATION NUMBER: US/10/000,439
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/847,208
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-439-2

Query Match 100.0%; Score 1764; DB 14; Length 330;
Best Local Similarity 100.0%; Pred. No. 1,1e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPVFPPLAPSSKSTSGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPVFPPLAPSSKSTSGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKHTHTCPCPAPPELLGG 120
Db 61 GLYSLSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKHTHTCPCPAPPELLGG 120
QY 121 PSVFLPPPKKDTLMISRPEVTCVVVDVSHEDPEVKFMWYDGVENHNVKTKRPREQYN 180
Db 121 PSVFLPPPKKDTLMISRPEVTCVVVDVSHEDPEVKFMWYDGVENHNVKTKRPREQYN 180
QY 181 STYRVVSVLTIVLHQMWMNGKEYCKVSNKALPAPIEKITSKAKVQPREQVYTLPPSRDE 240
Db 181 STYRVVSVLTIVLHQMWMNGKEYCKVSNKALPAPIEKITSKAKVQPREQVYTLPPSRDE 240
QY 241 LTRKNQVSLTCLVKGFPSPDIAVWESNNGOPENNYYKTPPVLDVSGSFFLYSKLTVDKSRW 300
Db 241 LTRKNQVSLTCLVKGFPSPDIAVWESNNGOPENNYYKTPPVLDVSGSFFLYSKLTVDKSRW 300
QY 301 OQGNVFSCSVMHGALHNHYQQRSLSLSPGK 330
Db 301 OQGNVFSCSVMHGALHNHYQQRSLSLSPGK 330

RESULT 3
US-09-995-898A-15
; Sequence 15, Application US/09995898A
; Publication No. US20030027253A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng
; APPLICANT: No. US20030027253A1ak, Julia E.
```

```
; APPLICANT: Whitmore, Theodore E.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
; FILE REFERENCE: 00-108
; CURRENT APPLICATION NUMBER: US/09/995,898A
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/253,561
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/267,211
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-995-898A-15

Query Match 98.0%; Score 1729; DB 10; Length 330;
Best Local Similarity 97.9%; Pred. No. 5,9e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPVFPPLAPSSKSTSGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPVFPPLAPSSKSTSGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKHTHTCPCPAPPELLGG 120
Db 61 GLYSLSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKHTHTCPCPAPPELLGG 120
QY 121 PSVFLPPPKKDTLMISRPEVTCVVVDVSHEDPEVKFMWYDGVENHNVKTKRPREQYN 180
Db 121 PSVFLPPPKKDTLMISRPEVTCVVVDVSHEDPEVKFMWYDGVENHNVKTKRPREQYN 180
QY 181 STYRVVSVLTIVLHQMWMNGKEYCKVSNKALPAPIEKITSKAKVQPREQVYTLPPSRDE 240
Db 181 STYRVVSVLTIVLHQMWMNGKEYCKVSNKALPAPIEKITSKAKVQPREQVYTLPPSRDE 240
QY 241 LTRKNQVSLTCLVKGFPSPDIAVWESNNGOPENNYYKTPPVLDVSGSFFLYSKLTVDKSRW 300
Db 241 LTRKNQVSLTCLVKGFPSPDIAVWESNNGOPENNYYKTPPVLDVSGSFFLYSKLTVDKSRW 300
QY 301 OQGNVFSCSVMHGALHNHYQQRSLSLSPGK 330
Db 301 OQGNVFSCSVMHGALHNHYQQRSLSLSPGK 330

RESULT 4
US-09-892-949-38
; Sequence 38, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Geo, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuljper, Joseph L.
; APPLICANT: Maurel, Joseph L.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 330
; TYPE: PRT
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ORGANISM: Homo sapiens  
US-09-892-949-38

Query Match  
Best Local Similarity 98.0%; Score 1729; DB 10; Length 330;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSPVPLAPSSKSTSGGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
DB 1 ASTKGPSPVPLAPSSKSTSGGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
QY 61 GLYSLSVVTVSSSSISGTQTYICNVNHNKSNKTVDKKVPKSCDKHTHTCPCPAPRLGG 120  
DB 61 GLYSLSVVTVSSSSISGTQTYICNVNHNKSNKTVDKKVPKSCDKHTHTCPCPAPRLGG 120  
QY 121 PSVFLPFPKPKDTLMTSRPEVTCVVDVSHEDPEVKFMVYDGVVHNAKTKPREQYN 180  
DB 121 PSVFLPFPKPKDTLMTSRPEVTCVVDVSHEDPEVKFMVYDGVVHNAKTKPREQYN 180  
QY 181 STYRVSVLTVLHQNMMNGEKYCKVSNKALPAPIEKTISKAKGQPREQVYTLPPSRDE 240  
DB 181 STYRVSVLTVLHQNMMNGEKYCKVSNKALPAPIEKTISKAKGQPREQVYTLPPSRDE 240  
QY 241 LTRKQVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW 300  
DB 241 LTRKQVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW 300  
QY 301 OQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330  
DB 301 OQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330

## RESULT 5

US-10-047-542-20  
Sequence 20, Application US/10047542  
Publication No. US20020168367A1  
GENERAL INFORMATION:  
APPLICANT: LARRICK, JAMES W.  
APPLICANT: WYCOFF, KEITH L.  
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL  
TITLE OF INVENTION: AND BACTERIAL DISEASES  
FILE REFERENCE: 030905, 0004, CIP1  
CURRENT APPLICATION NUMBER: US/10/047, 542  
CURRENT FILING DATE: 2001-10-26  
PRIOR APPLICATION NUMBER: PCT/US01/13932  
PRIOR FILING DATE: 2001-04-28  
PRIOR APPLICATION NUMBER: 60/200, 298  
NUMBER OF SEQ ID NOS: 101  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 20  
LENGTH: 330  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-047-542-20

Query Match  
Best Local Similarity 97.9%; Score 1729; DB 13; Length 330;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSPVPLAPSSKSTSGGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
DB 1 ASTKGPSPVPLAPSSKSTSGGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
QY 61 GLYSLSVVTVSSSSISGTQTYICNVNHNKSNKTVDKKVPKSCDKHTHTCPCPAPRLGG 120  
DB 61 GLYSLSVVTVSSSSISGTQTYICNVNHNKSNKTVDKKVPKSCDKHTHTCPCPAPRLGG 120  
QY 121 PSVFLPFPKPKDTLMTSRPEVTCVVDVSHEDPEVKFMVYDGVVHNAKTKPREQYN 180  
DB 121 PSVFLPFPKPKDTLMTSRPEVTCVVDVSHEDPEVKFMVYDGVVHNAKTKPREQYN 180  
QY 181 STYRVSVLTVLHQNMMNGEKYCKVSNKALPAPIEKTISKAKGQPREQVYTLPPSRDE 240

DB 181 STYRVSVLTVLHQNMMNGEKYCKVSNKALPAPIEKTISKAKGQPREQVYTLPPSRDE 240  
QY 241 LTRKQVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW 300  
DB 241 LTRKQVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW 300  
QY 301 OQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330  
DB 301 OQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330

## RESULT 6

US-10-269-805-68  
Sequence 68, Application US/10269805  
Publication No. US20030124129A1  
GENERAL INFORMATION:  
APPLICANT: OLINER, JONATHAN D.  
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS  
FILE REFERENCE: A-722  
CURRENT APPLICATION NUMBER: US/10/269, 805  
CURRENT FILING DATE: 2002-10-10  
PRIOR APPLICATION NUMBER: US 60/328, 604  
PRIOR FILING DATE: 2001-10-11  
NUMBER OF SEQ ID NOS: 76  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 68  
LENGTH: 330  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-269-805-68

Query Match  
Best Local Similarity 98.0%; Score 1729; DB 14; Length 330;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSPVPLAPSSKSTSGGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
DB 1 ASTKGPSPVPLAPSSKSTSGGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
QY 61 GLYSLSVVTVSSSSISGTQTYICNVNHNKSNKTVDKKVPKSCDKHTHTCPCPAPRLGG 120  
DB 61 GLYSLSVVTVSSSSISGTQTYICNVNHNKSNKTVDKKVPKSCDKHTHTCPCPAPRLGG 120  
QY 121 PSVFLPFPKPKDTLMTSRPEVTCVVDVSHEDPEVKFMVYDGVVHNAKTKPREQYN 180  
DB 121 PSVFLPFPKPKDTLMTSRPEVTCVVDVSHEDPEVKFMVYDGVVHNAKTKPREQYN 180  
QY 181 STYRVSVLTVLHQNMMNGEKYCKVSNKALPAPIEKTISKAKGQPREQVYTLPPSRDE 240  
DB 181 STYRVSVLTVLHQNMMNGEKYCKVSNKALPAPIEKTISKAKGQPREQVYTLPPSRDE 240  
QY 241 LTRKQVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW 300  
DB 241 LTRKQVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW 300  
QY 301 OQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330  
DB 301 OQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330

## RESULT 7

US-10-310-719-8  
Sequence 8, Application US/10310719  
Publication No. US20030166163A1  
GENERAL INFORMATION:  
APPLICANT: GILLIES, STEPHEN  
TITLE OF INVENTION: IMMUNOCYTOKINES WITH MODULATED SELECTIVITY  
FILE REFERENCE: LEX-020  
CURRENT APPLICATION NUMBER: US/10/310, 719  
CURRENT FILING DATE: 2002-12-04  
PRIOR APPLICATION NUMBER: 60/337, 113  
PRIOR FILING DATE: 2001-12-04

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; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc
; LOCATION: (1)..(330)
; OTHER INFORMATION: IgG1 constant region
US-10-310-719-8

Query Match          98.0%; Score 1729; DB 14; Length 330;
Best Local Similarity 97.9%; Pred. No. 5.9e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAAAGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPPLAPSSKSTSGGTAAAGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 60

QY 61 GLYSLSVVTVPSSSLGTQTYICNNVHKPSNTKVDKVEPKSCDKHTHTCPPCPAPPELLGG 120
DB 61 GLYSLSVVTVPSSSLGTQTYICNNVHKPSNTKVDKVEPKSCDKHTHTCPPCPAPPELLGG 120

QY 121 PSVFLPPEPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYVDGVEVHNAKTKRPREQYN 180
DB 121 PSVFLPPEPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYVDGVEVHNAKTKRPREQYN 180

QY 181 STYRVVSVLTVLIHQWMNNGEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240
DB 181 STYRVVSVLTVLIHQWMNNGEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240

QY 241 LTKNOVSLTCLVKGFYPSDIAVEMESNGQPENNYKTPPVLDVSGSFPLYSKLTVDKSRW 300
DB 241 LTKNOVSLTCLVKGFYPSDIAVEMESNGQPENNYKTPPVLDVSGSFPLYSKLTVDKSRW 300

QY 301 QCGNVFSCSVMHREALHNNHYQQRSLSPGK 330
DB 301 QCGNVFSCSVMHREALHNNHYQQRSLSPGK 330

RESULT 8
US-10-112-582-1
; Sequence 1, Application US/10112582
; Publication No. US2003016687A1
; GENERAL INFORMATION:
; APPLICANT: Glilies, Stephen
; TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
; FILE REFERENCE: LEX-017
; CURRENT APPLICATION NUMBER: US/10/112,582
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/280,625
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: human Ig gamma heavy chain C region
US-10-112-582-1

Query Match          98.0%; Score 1729; DB 14; Length 330;
Best Local Similarity 97.9%; Pred. No. 5.9e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAAAGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPPLAPSSKSTSGGTAAAGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 60
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QY 61 GLYSLSVVTVPSSSLGTQTYICNNVHKPSNTKVDKVEPKSCDKHTHTCPPCPAPPELLGG 120
DB 61 GLYSLSVVTVPSSSLGTQTYICNNVHKPSNTKVDKVEPKSCDKHTHTCPPCPAPPELLGG 120

QY 121 PSVFLPPEPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYVDGVEVHNAKTKRPREQYN 180
DB 121 PSVFLPPEPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYVDGVEVHNAKTKRPREQYN 180

QY 181 STYRVVSVLTVLIHQWMNNGEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240
DB 181 STYRVVSVLTVLIHQWMNNGEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240

QY 241 LTKNOVSLTCLVKGFYPSDIAVEMESNGQPENNYKTPPVLDVSGSFPLYSKLTVDKSRW 300
DB 241 LTKNOVSLTCLVKGFYPSDIAVEMESNGQPENNYKTPPVLDVSGSFPLYSKLTVDKSRW 300

QY 301 QCGNVFSCSVMHREALHNNHYQQRSLSPGK 330
DB 301 QCGNVFSCSVMHREALHNNHYQQRSLSPGK 330
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RESULT 9
US-10-320-231A-81
; Sequence 81, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; FILE REFERENCE: 7430*163
; CURRENT APPLICATION NUMBER: US/10/320,231A
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,174
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 81
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-320-231A-81

Query Match          98.0%; Score 1729; DB 14; Length 330;
Best Local Similarity 97.9%; Pred. No. 5.9e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAAAGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPPLAPSSKSTSGGTAAAGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 60

QY 61 GLYSLSVVTVPSSSLGTQTYICNNVHKPSNTKVDKVEPKSCDKHTHTCPPCPAPPELLGG 120
DB 61 GLYSLSVVTVPSSSLGTQTYICNNVHKPSNTKVDKVEPKSCDKHTHTCPPCPAPPELLGG 120

QY 121 PSVFLPPEPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYVDGVEVHNAKTKRPREQYN 180
DB 121 PSVFLPPEPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYVDGVEVHNAKTKRPREQYN 180

QY 181 STYRVVSVLTVLIHQWMNNGEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240
DB 181 STYRVVSVLTVLIHQWMNNGEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240

QY 241 LTKNOVSLTCLVKGFYPSDIAVEMESNGQPENNYKTPPVLDVSGSFPLYSKLTVDKSRW 300
DB 241 LTKNOVSLTCLVKGFYPSDIAVEMESNGQPENNYKTPPVLDVSGSFPLYSKLTVDKSRW 300

QY 301 QCGNVFSCSVMHREALHNNHYQQRSLSPGK 330
DB 301 QCGNVFSCSVMHREALHNNHYQQRSLSPGK 330
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RESULT 10
US-10-383-902A-6
; Sequence 6, Application US/10383902A
; Publication No. US20030224408A1
GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Mullberg, Jurgen
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: LIGAND SCREENING AND DISCOVERY
; FILE REFERENCE: 10280-042001
; CURRENT APPLICATION NUMBER: US/10/383,902A
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/362,403
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated plasmid sequence
US-10-383-902A-6

Query Match          98.0%; Score 1729; DB 15; Length 330;
Best Local Similarity 97.9%; Pred. No. 5.9e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTGSPVPLAPSSKSTSGGTALGCLVKDYFPEPVYTSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTGSPVPLAPSSKSTSGGTALGCLVKDYFPEPVYTSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVSSSLGTQTYICNVNHRKPSNTKVDKVPKSCDKHTHCPCPAPRLGG 120
DB 61 GLYSLSVVTVSSSLGTQTYICNVNHRKPSNTKVDKVPKSCDKHTHCPCPAPRLGG 120
QY 121 PSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVGVNNAVTKPREQYN 180
DB 121 PSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVGVNNAVTKPREQYN 180
QY 181 STYRVVSVLTVLIHQMNGEKYCKVSNKALPAPIEKTIISKAKGPREPQVYTLPPSRDE 240
DB 181 STYRVVSVLTVLIHQMNGEKYCKVSNKALPAPIEKTIISKAKGPREPQVYTLPPSRDE 240
QY 241 LTRKQVSLTCLVKGFPYPSDIAVWESNQPENNYKTTTPVLDSGSPFLYSKLTVDKSRW 300
DB 241 LTRKQVSLTCLVKGFPYPSDIAVWESNQPENNYKTTTPVLDSGSPFLYSKLTVDKSRW 300
QY 301 QOGNVFSCVMHEALHNHYQOQSLSLSPGK 330
DB 301 QOGNVFSCVMHEALHNHYQOQSLSLSPGK 330

RESULT 11
US-10-408-901-2
; Sequence 2, Application US/10408901
; Publication No. US20040023313A1
GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Huang, Haichun
; APPLICANT: Eliot, Robin
; APPLICANT: Sullivan, John
; APPLICANT: Medlock, Eugene
; APPLICANT: Martin, Francis
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
; FILE REFERENCE: MHB 01-1145-A
; CURRENT APPLICATION NUMBER: US/10/408,901
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
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; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-901-2

Query Match          98.0%; Score 1729; DB 15; Length 330;
Best Local Similarity 97.9%; Pred. No. 5.9e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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DB 61 GLYSLSVVTVSSSLGTQTYICNVNHRKPSNTKVDKVPKSCDKHTHCPCPAPRLGG 120
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DB 121 PSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVGVNNAVTKPREQYN 180
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DB 181 STYRVVSVLTVLIHQMNGEKYCKVSNKALPAPIEKTIISKAKGPREPQVYTLPPSRDE 240
QY 241 LTRKQVSLTCLVKGFPYPSDIAVWESNQPENNYKTTTPVLDSGSPFLYSKLTVDKSRW 300
DB 241 LTRKQVSLTCLVKGFPYPSDIAVWESNQPENNYKTTTPVLDSGSPFLYSKLTVDKSRW 300
QY 301 QOGNVFSCVMHEALHNHYQOQSLSLSPGK 330
DB 301 QOGNVFSCVMHEALHNHYQOQSLSLSPGK 330

RESULT 12
US-10-420-034A-15
; Sequence 15, Application US/10420034A
; Publication No. US20040029228A1
GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng
; APPLICANT: No. US20040029228A1ak, Julia E.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Grant, Francis J.
; APPLICANT: Klueber, Kevin M.
; APPLICANT: Klueber, Kevin M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; FILE REFERENCE: 02-10
; CURRENT APPLICATION NUMBER: US/10/420,034A
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 60/373,813
; PRIOR FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-420-034A-15

Query Match          98.0%; Score 1729; DB 15; Length 330;
Best Local Similarity 97.9%; Pred. No. 5.9e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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DB 1 ASTGSPVPLAPSSKSTSGGTALGCLVKDYFPEPVYTSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVSSSLGTQTYICNVNHRKPSNTKVDKVPKSCDKHTHCPCPAPRLGG 120
DB 61 GLYSLSVVTVSSSLGTQTYICNVNHRKPSNTKVDKVPKSCDKHTHCPCPAPRLGG 120
QY 121 PSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVGVNNAVTKPREQYN 180
DB 121 PSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVGVNNAVTKPREQYN 180
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Db 181 STYRVSVLTVLHQMNMNGKEYCKKVSNAKALPAPIEKTISKAKVQPREQVYTLPPSRDE 240
Qy 241 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFLYSKLTVDKSRW 300
Db 241 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFLYSKLTVDKSRW 300
Qy 301 QQGNVFSCSVMEHALHNHYQORSLSLSPGK 330
Db 301 QQGNVFSCSVMEHALHNHYTQKSLSLSPGK 330

RESULT 13
US-10-257-907-5
; Sequence 5, Application US/10257907
; Publication No. US20040043022A1
; GENERAL INFORMATION:
; APPLICANT: Heuer, Josef
; APPLICANT: Liu, Jingqi
; APPLICANT: Na, Songqing
; APPLICANT: Song, Ho Yeong
; APPLICANT: Yang, Derek Di
; TITLE OF INVENTION: TREATING T-CELL MEDIATED DISEASES BY MODULATING DR6 ACTIVITY
; FILE REFERENCE: X-13992
; CURRENT APPLICATION NUMBER: US/10/257,907
; CURRENT FILING DATE: 2002-10-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent version 3.0
; SEQ ID NO 5
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-257-907-5

Query Match 98.0%; Score 1729; DB 15; Length 330;
Best Local Similarity 97.9%; Pred. No. 5.9e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPVSFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 60
Db 1 ASTKGPVSFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSVTVTPSSSLGTQTYICNVNHRPSNTKVDKVEPKSCDKHTHTCPCPAPPELLGG 120
Db 61 GLYSLSVTVTPSSSLGTQTYICNVNHRPSNTKVDKVEPKSCDKHTHTCPCPAPPELLGG 120
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Db 121 PSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVENNAKTKPREEQYN 180
Qy 181 STYRVSVLTVLHQMNMNGKEYCKKVSNAKALPAPIEKTISKAKVQPREQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQMNMNGKEYCKKVSNAKALPAPIEKTISKAKVQPREQVYTLPPSRDE 240
Qy 241 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFLYSKLTVDKSRW 300
Db 241 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFLYSKLTVDKSRW 300
Qy 301 QQGNVFSCSVMEHALHNHYQORSLSLSPGK 330
Db 301 QQGNVFSCSVMEHALHNHYTQKSLSLSPGK 330

RESULT 14
US-10-656-769-2
; Sequence 2, Application US/10656769
; Publication No. US20040097712A1
; GENERAL INFORMATION:
; APPLICANT: Varnum, Brian
```

```
; APPLICANT: Witte, Alison
; APPLICANT: Wezina, Chris
; APPLICANT: Wong, Lu Min
; APPLICANT: Qian, Xueming
; TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody
; FILE REFERENCE: 01,1554
; CURRENT APPLICATION NUMBER: US/10/656,769
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Patent version 3.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-656-769-2

Query Match 98.0%; Score 1729; DB 15; Length 330;
Best Local Similarity 97.9%; Pred. No. 5.9e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPVSFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 60
Db 1 ASTKGPVSFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSVTVTPSSSLGTQTYICNVNHRPSNTKVDKVEPKSCDKHTHTCPCPAPPELLGG 120
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Db 121 PSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVENNAKTKPREEQYN 180
Qy 181 STYRVSVLTVLHQMNMNGKEYCKKVSNAKALPAPIEKTISKAKVQPREQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQMNMNGKEYCKKVSNAKALPAPIEKTISKAKVQPREQVYTLPPSRDE 240
Qy 241 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFLYSKLTVDKSRW 300
Db 241 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFLYSKLTVDKSRW 300
Qy 301 QQGNVFSCSVMEHALHNHYQORSLSLSPGK 330
Db 301 QQGNVFSCSVMEHALHNHYTQKSLSLSPGK 330

RESULT 15
US-10-772-531-38
; Sequence 38, Application US/10772531
; Publication No. US20040142422A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Preenell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/10/772,531
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US/09/892,949
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 330
; TYPE: PRT
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; ORGANISM: Homo sapiens  
US-10-772-531-38

Query Match 98.0%; Score 1729; DB 16; Length 330;  
Best Local Similarity 97.9%; Pred. No. 5, 9e-126;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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      1 ASTKGSPVPLAPSSKSTSGGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db
QY      61 GLYSLSVVTVTPSSSLGTOTYICNVNHNKSNNTKVDKKVEPKSCDKTHTCPCPCAPELLGG 120
      61 GLYSLSVVTVTPSSSLGTOTYICNVNHNKSNNTKVDKKVEPKSCDKTHTCPCPCAPELLGG 120
Db
QY      121 PSVFLFPPPKDITLMTSRTPEVTGVVDVSHEDPEYKFNMYVDGVEVHNKTKPREEOYN 180
      121 PSVFLFPPPKDITLMTSRTPEVTGVVDVSHEDPEYKFNMYVDGVEVHNKTKPREEOYN 180
Db
QY      181 STYRVVSVLTVLHQMMNGKEYKCKVSNKALPAPIEKTIISKAKQPREPOVYTLPPSRDE 240
      181 STYRVVSVLTVLHQMMNGKEYKCKVSNKALPAPIEKTIISKAKQPREPOVYTLPPSRDE 240
Db
QY      241 LTRNQVSLTCLVKGFPSPDIAYEMESNGQPENNYKTTTPVLDVSGSFLLYSKLTVDKSRW 300
      241 LTRNQVSLTCLVKGFPSPDIAYEMESNGQPENNYKTTTPVLDVSGSFLLYSKLTVDKSRW 300
Db
QY      301 OQGNVFCSVMEHALHNHYQORSLSLSPGK 330
      301 OQGNVFCSVMEHALHNHYTOKSLSLSPGK 330
Db
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Search completed: June 7, 2005, 09:25:06  
Job time : 145.767 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 08:49:07 ; Search time 46.1658 Seconds  
(without alignments)  
533.603 Million cell updates/sec

Title: US-10-000-439-2

Perfect score: 1764

Sequence: 1 ASTKGPVFPPLAPSSKSTSG.....MHEALHNHYQQRSLSPGK 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA:\*  
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2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/6C\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	1729	98.0	371	1	US-08-236-311-7
2	1729	98.0	371	3	US-08-457-918-7
3	1729	98.0	371	4	US-10-157-408-7
4	1729	98.0	446	3	US-08-397-411-7
5	1729	98.0	449	1	US-08-458-516-13
6	1729	98.0	467	4	US-08-030-175-41
7	1729	98.0	467	4	US-08-030-175-42
8	1729	98.0	476	2	US-08-378-939-10
9	1729	98.0	547	4	US-09-746-359A-54
10	1729	98.0	567	4	US-09-825-561A-16
11	1729	98.0	571	4	US-09-746-359B-53
12	1729	98.0	951	4	US-09-313-942-9
13	1725	97.8	462	4	US-09-289-942A-7
14	1725	97.8	476	3	US-09-740-002-27
15	1725	97.8	476	3	US-08-487-550-4
16	1725	97.8	476	3	US-08-487-550-12
17	1725	97.8	476	4	US-09-526-098-4
18	1725	97.8	476	4	US-09-526-098-12
19	1725	97.8	476	4	US-09-383-916-4
20	1725	97.8	476	4	US-08-487-550-8
21	1725	97.8	478	3	US-08-487-550-12
22	1725	97.8	478	3	US-09-526-098-8
23	1725	97.8	478	4	US-09-383-916-8
24	1724	97.7	459	1	US-08-157-101A-7
25	1724	97.7	475	4	US-09-740-002-25
26	1723	97.7	330	4	US-09-301-593-22
27	1723	97.7	451	2	US-08-887-352B-14

28	1723	97.7	451	2	US-08-887-352B-16	Sequence 16, Appl
29	1723	97.7	451	2	US-08-887-352B-18	Sequence 18, Appl
30	1723	97.7	451	3	US-08-466-151-65	Sequence 65, Appl
31	1723	97.7	451	3	US-09-109-207C-14	Sequence 14, Appl
32	1723	97.7	451	3	US-09-109-207C-16	Sequence 16, Appl
33	1723	97.7	451	3	US-09-109-207C-18	Sequence 18, Appl
34	1723	97.7	451	3	US-09-282-505-2	Sequence 2, Appl
35	1723	97.7	451	3	US-09-054-255-2	Sequence 2, Appl
36	1723	97.7	451	3	US-09-296-005-14	Sequence 14, Appl
37	1723	97.7	451	3	US-09-296-005-16	Sequence 16, Appl
38	1723	97.7	451	3	US-09-296-005-18	Sequence 18, Appl
39	1723	97.7	451	4	US-09-282-846-2	Sequence 2, Appl
40	1723	97.7	451	4	US-09-680-145-2	Sequence 2, Appl
41	1723	97.7	451	4	US-09-920-171-14	Sequence 14, Appl
42	1723	97.7	451	4	US-09-920-171-16	Sequence 16, Appl
43	1723	97.7	451	4	US-09-920-171-18	Sequence 18, Appl
44	1723	97.7	451	4	US-09-716-028-14	Sequence 14, Appl
45	1723	97.7	451	4	US-09-716-028-16	Sequence 16, Appl

#### ALIGNMENTS

RESULT 1  
US-08-236-311-7  
; Sequence 7, Application US/08236311  
; Patent No. 5565335  
; GENERAL INFORMATION:  
; APPLICANT: Capon, Daniel J.  
; APPLICANT: Gregory, Timothy J.  
; TITLE OF INVENTION: Adhesion Variants  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/236,311  
; FILING DATE: 02-MAY-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/936190  
; FILING DATE: 26-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/842777  
; FILING DATE: 18-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/250785  
; FILING DATE: 28-SEP-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/104329  
; FILING DATE: 02-OCT-1987  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 444PIC2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1996  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 371 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

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US-08-236-311-7
Query Match          98.0%; Score 1729; DB 1; Length 371;
Best Local Similarity 97.9%; Pred. No. 3.2e-157;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSPVPLAPSSKSTSGGTAALGCLVKDYFPEPVYVSNMNSGALTSGVHTFPAVLQSS 60
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QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPPELLGG 120
DB 102 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPPELLGG 161
QY 121 PSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFMWYDGEVHNHAKTKPREEQYN 180
DB 162 PSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFMWYDGEVHNHAKTKPREEQYN 221
QY 181 STYRVSVVLTIVLHQMNGKEKCKVSNKALPAPIEKITSKAKVQPREQVYVTLPPSRDE 240
DB 222 STYRVSVVLTIVLHQMNGKEKCKVSNKALPAPIEKITSKAKVQPREQVYVTLPPSRDE 281
QY 241 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDVSGSFPLYSLKLTVDKSRW 300
DB 282 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDVSGSFPLYSLKLTVDKSRW 341
QY 301 QOQNVFSCSVMEALHNHYQORSLSLSPGK 330
DB 342 QOQNVFSCSVMEALHNHYQORSLSLSPGK 371

RESULT 2
US-08-457-918-7
; Sequence 7, Application US/08457918
; Patent No. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457, 918
; FILING DATE: 1-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubic, Jeffrey S.
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REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0444P1C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-457-918-7
Query Match          98.0%; Score 1729; DB 3; Length 371;
Best Local Similarity 97.9%; Pred. No. 3.2e-157;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPPELLGG 120
DB 102 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPPELLGG 161
QY 121 PSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFMWYDGEVHNHAKTKPREEQYN 180
DB 162 PSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFMWYDGEVHNHAKTKPREEQYN 221
QY 181 STYRVSVVLTIVLHQMNGKEKCKVSNKALPAPIEKITSKAKVQPREQVYVTLPPSRDE 240
DB 222 STYRVSVVLTIVLHQMNGKEKCKVSNKALPAPIEKITSKAKVQPREQVYVTLPPSRDE 281
QY 241 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDVSGSFPLYSLKLTVDKSRW 300
DB 282 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPVLDVSGSFPLYSLKLTVDKSRW 341
QY 301 QOQNVFSCSVMEALHNHYQORSLSLSPGK 330
DB 342 QOQNVFSCSVMEALHNHYQORSLSLSPGK 371

RESULT 3
US-10-157-408-7
; Sequence 7, Application US/10157408
; Patent No. 6710169
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/157,408
; FILING DATE: 28-May-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 07/936190
```

FILING DATE: 26-AUG-1992  
APPLICATION NUMBER: 07/842777  
FILING DATE: 18-FEB-1992  
APPLICATION NUMBER: 07/250785  
FILING DATE: 28-SEP-1988  
APPLICATION NUMBER: 07/104329  
FILING DATE: 02-OCT-1967  
ATTORNEY/AGENT INFORMATION:  
NAME: Kubinec, Jeffrey S.  
REGISTRATION NUMBER: 36,575  
REFERENCE/DOCKET NUMBER: P0444PIC3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8228  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 371 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-157-408-7

Query Match 98.0%; Score 1729; DB 4; Length 371;  
Best Local Similarity 97.9%; Pred. No. 3.2e-157;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPVPLAPSSKSTSGTALGCLVKDYFPEPVTVSNMGSALTSGVHFPAYLQSS 60  
DB 42 ASTKGPVPLAPSSKSTSGTALGCLVKDYFPEPVTVSNMGSALTSGVHFPAYLQSS 101  
QY 61 GLYSLSVTVTVSSSLGTQTYICNVNPKSNTKVDKVEPKSCDKHTCTPCAPAPLLGG 120  
DB 102 GLYSLSVTVTVSSSLGTQTYICNVNPKSNTKVDKVEPKSCDKHTCTPCAPAPLLGG 161  
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVVHNAKTKPREEOYN 180  
DB 162 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVVHNAKTKPREEOYN 221  
QY 181 STYRVSVTLTVLHOMNMGKEYCKVSNKALPAPIEKTIISKAVQPREPOVYTLPPSRDE 240  
DB 222 STYRVSVTLTVLHOMNMGKEYCKVSNKALPAPIEKTIISKAVQPREPOVYTLPPSRDE 281  
QY 241 LTRNQVSLTCLVKGFPSDIAVWESNGQPENNYKTPPVLDVSGSFPLYSKLTVDKSRW 300  
DB 282 LTRNQVSLTCLVKGFPSDIAVWESNGQPENNYKTPPVLDVSGSFPLYSKLTVDKSRW 341  
QY 301 QOQNVFSCVMHEALHNHYQOQSLSLSPGK 330  
DB 342 QOQNVFSCVMHEALHNHYQOQSLSLSPGK 371

RESULT 4  
US-08-397-411-7  
Sequence 7, Application US/08397411  
Patent No. 6129914  
GENERAL INFORMATION:  
APPLICANT: Weiner, George  
APPLICANT: Gingrich, Roger  
APPLICANT: Link, Brian  
APPLICANT: Teo, J. Yun  
TITLE OF INVENTION: Bispecific Antibody Effective to Treat  
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,411  
FILING DATE: 01-MAR-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/859,583  
FILING DATE: 27-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 011823-004901  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 446 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-397-411-7

Query Match 98.0%; Score 1729; DB 3; Length 446;  
Best Local Similarity 97.9%; Pred. No. 4.2e-157;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPVPLAPSSKSTSGTALGCLVKDYFPEPVTVSNMGSALTSGVHFPAYLQSS 60  
DB 117 ASTKGPVPLAPSSKSTSGTALGCLVKDYFPEPVTVSNMGSALTSGVHFPAYLQSS 176  
QY 61 GLYSLSVTVTVSSSLGTQTYICNVNPKSNTKVDKVEPKSCDKHTCTPCAPAPLLGG 120  
DB 177 GLYSLSVTVTVSSSLGTQTYICNVNPKSNTKVDKVEPKSCDKHTCTPCAPAPLLGG 236  
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVVHNAKTKPREEOYN 180  
DB 237 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGVVHNAKTKPREEOYN 296  
QY 181 STYRVSVTLTVLHOMNMGKEYCKVSNKALPAPIEKTIISKAVQPREPOVYTLPPSRDE 240  
DB 297 STYRVSVTLTVLHOMNMGKEYCKVSNKALPAPIEKTIISKAVQPREPOVYTLPPSRDE 356  
QY 241 LTRNQVSLTCLVKGFPSDIAVWESNGQPENNYKTPPVLDVSGSFPLYSKLTVDKSRW 300  
DB 357 LTRNQVSLTCLVKGFPSDIAVWESNGQPENNYKTPPVLDVSGSFPLYSKLTVDKSRW 416  
QY 301 QOQNVFSCVMHEALHNHYQOQSLSLSPGK 330  
DB 417 QOQNVFSCVMHEALHNHYQOQSLSLSPGK 446

RESULT 5  
US-08-458-516-13  
Sequence 13, Application US/08458516  
Patent No. 5777085  
GENERAL INFORMATION:  
APPLICANT: Co, Man Sung  
APPLICANT: Teo, J. Yun  
TITLE OF INVENTION: Humanized Antibodies Reactive with  
TITLE OF INVENTION: GRIB/IIIA  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSER: William M. Smith  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Releasee #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458,516  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/059,159  
FILING DATE: 03-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-37-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 449 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-458-516-13

Query Match 98.0%; Score 1729; DB 1; Length 449;  
Best Local Similarity 97.9%; Pred. No. 4.3e-157;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSPVPLAPSSKSTSGTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 60  
DB 120 ASTKGPSPVPLAPSSKSTSGTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 179  
QY 61 GLYSLSVTVTVSSSLGQTQYICNNHNRKSNKVDKVEPKSCDTHCTPCPAPPELLGG 120  
DB 180 GLYSLSVTVTVSSSLGQTQYICNNHNRKSNKVDKVEPKSCDTHCTPCPAPPELLGG 239  
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFMWYDGVENVHVKTKRPREQYN 180  
DB 240 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFMWYDGVENVHNAKTKRPREQYN 299  
QY 300 STYRVVSVLTVLHQMWNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359  
DB 241 LTRKQVSLTCLVKGFPSDIAVEMESNGQPENNYKTTPVLDSGSEFLYSKLTVDKSRW 300  
QY 360 LTRKQVSLTCLVKGFPSDIAVEMESNGQPENNYKTTPVLDSGSEFLYSKLTVDKSRW 419  
DB 301 QQGNVFCSCVMHEALHNHYQORSLSLSPGK 330  
QY 420 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449

RESULT 6  
US-08-030-175-41  
Sequence 41, Application US/08030175  
Patent No. 6767996  
GENERAL INFORMATION:  
APPLICANT: Gorman, Scott D.  
APPLICANT: Clark, Michael R.  
APPLICANT: Cobbold, Stephen P.  
APPLICANT: Waldmann, Herman  
TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.  
STREET: 555 13TH ST., NW, Suite 701 East  
CITY: Washington  
STATE: D. C.  
COUNTRY: U.S.

ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk, 5.25 inch, 360 Kb storage  
COMPUTER: IBM AT compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2  
SOFTWARE: Wordperfect 5.0 (Dos Text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/030,175  
FILING DATE: 17-MAY-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB91/01578  
FILING DATE: 13-SEP-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Ernst, Barbara G.  
REGISTRATION NUMBER: 30,377  
REFERENCE/DOCKET NUMBER: 1768-113  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)783-6040  
TELEFAX: (202)783-6031  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 467 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-030-175-41

Query Match 98.0%; Score 1729; DB 4; Length 467;  
Best Local Similarity 97.9%; Pred. No. 4.5e-157;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSPVPLAPSSKSTSGTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 60  
DB 138 ASTKGPSPVPLAPSSKSTSGTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 197  
QY 61 GLYSLSVTVTVSSSLGQTQYICNNHNRKSNKVDKVEPKSCDTHCTPCPAPPELLGG 120  
DB 198 GLYSLSVTVTVSSSLGQTQYICNNHNRKSNKVDKVEPKSCDTHCTPCPAPPELLGG 257  
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFMWYDGVENVHVKTKRPREQYN 180  
DB 258 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFMWYDGVENVHNAKTKRPREQYN 317  
QY 181 STYRVVSVLTVLHQMWNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
DB 318 STYRVVSVLTVLHQMWNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 377  
QY 241 LTRKQVSLTCLVKGFPSDIAVEMESNGQPENNYKTTPVLDSGSEFLYSKLTVDKSRW 300  
DB 378 LTRKQVSLTCLVKGFPSDIAVEMESNGQPENNYKTTPVLDSGSEFLYSKLTVDKSRW 437  
QY 301 QQGNVFCSCVMHEALHNHYQORSLSLSPGK 330  
DB 438 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 467

RESULT 7  
US-08-030-175-42  
Sequence 42, Application US/08030175  
Patent No. 6767996  
GENERAL INFORMATION:  
APPLICANT: Gorman, Scott D.  
APPLICANT: Clark, Michael R.  
APPLICANT: Cobbold, Stephen P.  
APPLICANT: Waldmann, Herman  
TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.  
STREET: 555 13TH ST., NW, Suite 701 East  
CITY: Washington  
STATE: D. C.

COUNTRY: U.S.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage  
COMPUTER: IBM AT compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2  
SOFTWARE: WordPerfect 5.0 (dos text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/030,175  
FILING DATE: 17-MAY-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB91/01578  
FILING DATE: 13-SEP-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Ernst, Barbara G.  
REGISTRATION NUMBER: 30,377  
REFERENCE/DOCKET NUMBER: 1768-113  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 783-6040  
TELEFAX: (202) 783-6031  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 467 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-030-175-42

Query Match 98.0%; Score 1729; DB 4; Length 467;  
Best Local Similarity 97.9%; Pred. No. 4.5e-157;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 ASTKGSVPFLPAPSSKSTSGTAAAGCLVKDYFPEPVYTMNMSGALTSVHTFPAVLQSS 60  
DB 138 ASTKGSVPFLPAPSSKSTSGTAAAGCLVKDYFPEPVYTMNMSGALTSVHTFPAVLQSS 197  
QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPPELLGG 120  
DB 198 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPPELLGG 257  
QY 121 PSVFLPPEPKDTLMISRTPEVTCVVDVSHEDPEVKFMWYDGVGVNNAKTKPREEQYN 180  
DB 258 PSVFLPPEPKDTLMISRTPEVTCVVDVSHEDPEVKFMWYDGVGVNNAKTKPREEQYN 317  
QY 181 STYRVSVTLVHQMNMNKEKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
DB 338 STYRVSVTLVHQMNMNKEKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 377  
QY 241 LTRKNQVSLTCLVKGFPSPDIAVWESNNGOPENNYKTTTPVLDSVGSFFLYSKLTVDKSRM 300  
DB 378 LTRKNQVSLTCLVKGFPSPDIAVWESNNGOPENNYKTTTPVLDSVGSFFLYSKLTVDKSRM 437  
QY 301 QOQNVFSCSVMEHALHNHYQQRSLSLSPGK 330  
DB 438 QOQNVFSCSVMEHALHNHYQQRSLSLSPGK 467

RESULT 8  
US-08-378-939-10  
Sequence 10, Application US/08378939  
Patent No. 5876961  
GENERAL INFORMATION:  
APPLICANT: CROME, JAMES SCOTT  
APPLICANT: LEWIS, ALAN PETER  
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ  
STREET: 555 THIRTEENTH ST. N.W.  
CITY: WASHINGTON  
STATE: D. C.  
COUNTRY: U. S.

ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/378,939  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/952640  
FILING DATE: 01-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: ERNST, BARBARA G.  
REGISTRATION NUMBER: 30,377  
REFERENCE/DOCKET NUMBER: 1808-118  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 783-6040  
TELEFAX: (202) 783-6031  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 476 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-378-939-10

Query Match 98.0%; Score 1729; DB 2; Length 476;  
Best Local Similarity 97.9%; Pred. No. 4.7e-157;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 ASTKGSVPFLPAPSSKSTSGTAAAGCLVKDYFPEPVYTMNMSGALTSVHTFPAVLQSS 60  
DB 147 ASTKGSVPFLPAPSSKSTSGTAAAGCLVKDYFPEPVYTMNMSGALTSVHTFPAVLQSS 206  
QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPPELLGG 120  
DB 207 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPPELLGG 266  
QY 121 PSVFLPPEPKDTLMISRTPEVTCVVDVSHEDPEVKFMWYDGVGVNNAKTKPREEQYN 180  
DB 267 PSVFLPPEPKDTLMISRTPEVTCVVDVSHEDPEVKFMWYDGVGVNNAKTKPREEQYN 326  
QY 181 STYRVSVTLVHQMNMNKEKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
DB 327 STYRVSVTLVHQMNMNKEKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386  
QY 241 LTRKNQVSLTCLVKGFPSPDIAVWESNNGOPENNYKTTTPVLDSVGSFFLYSKLTVDKSRM 300  
DB 387 LTRKNQVSLTCLVKGFPSPDIAVWESNNGOPENNYKTTTPVLDSVGSFFLYSKLTVDKSRM 446  
QY 301 QOQNVFSCSVMEHALHNHYQQRSLSLSPGK 330  
DB 447 QOQNVFSCSVMEHALHNHYQQRSLSLSPGK 476

RESULT 9  
US-09-746-359A-54  
Sequence 54, Application US/09746359A  
Patent No. 6610286  
GENERAL INFORMATION:  
APPLICANT: Thompson, Penny  
APPLICANT: Foster, Donald C.  
APPLICANT: Xu, Wenfeng  
APPLICANT: Madden, Karen L.  
APPLICANT: Kelly, James D.  
APPLICANT: Sprecher, Cindy A.  
APPLICANT: Blumberg, Hal  
APPLICANT: Eagan, Maribeth A.  
APPLICANT: Jaspers, Stephen R.  
APPLICANT: Chandrasekhar, Yamin A.  
APPLICANT: No. 6610286ak, Julia E.

```

; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-746-359A-54

Query Match          98.0%; Score 1729; DB 4; Length 547;
Best Local Similarity 97.9%; Pred. No. 5,7e-157;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1  ASTKPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNMNSGALTSGVHTFPAVLQSS 60
        |||
DB      218  ASTKPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNMNSGALTSGVHTFPAVLQSS 277
        |||

QY      61  GLYSLSVVTVPSSSLGTQTYICNNHKPSNTKVDKVEPKSCDKTHPCPCPAPPELLGG 120
        |||
DB      278  GLYSLSVVTVPSSSLGTQTYICNNHKPSNTKVDKVEPKSCDKTHPCPCPAPPELLGG 337
        |||

QY      121  PSVFLPPEPKDITLMSRTPEVTCVVVDVSHEDPEVKFMWYDGVENNAKTKPREEOYN 180
        |||
DB      338  PSVFLPPEPKDITLMSRTPEVTCVVVDVSHEDPEVKFMWYDGVENNAKTKPREEOYN 397
        |||

QY      181  STYRVSVLTIVLHQMNGKEKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
        |||
DB      398  STYRVSVLTIVLHQMNGKEKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 457
        |||

QY      241  LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
        |||
DB      458  LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 517
        |||

QY      301  QOQNVFSCSVMEALAHNYQORSLSLSPGK 330
        |||
DB      518  QOQNVFSCSVMEALAHNYQORSLSLSPGK 547
        |||

RESULT 10
US-09-825-561A-16
; Sequence 16, Application US/09825561A
; Patent No. 6777539
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. 6777539ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: soluble zalphallR/IgGgamma1 polypeptide
US-09-825-561A-16
```

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Query Match          98.0%; Score 1729; DB 4; Length 567;
Best Local Similarity 97.9%; Pred. No. 6.1e-157;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1  ASTKPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNMNSGALTSGVHTFPAVLQSS 60
        |||
DB      238  ASTKPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNMNSGALTSGVHTFPAVLQSS 297
        |||

QY      61  GLYSLSVVTVPSSSLGTQTYICNNHKPSNTKVDKVEPKSCDKTHPCPCPAPPELLGG 120
        |||
DB      238  GLYSLSVVTVPSSSLGTQTYICNNHKPSNTKVDKVEPKSCDKTHPCPCPAPPELLGG 357
        |||

QY      121  PSVFLPPEPKDITLMSRTPEVTCVVVDVSHEDPEVKFMWYDGVENNAKTKPREEOYN 180
        |||
DB      358  PSVFLPPEPKDITLMSRTPEVTCVVVDVSHEDPEVKFMWYDGVENNAKTKPREEOYN 417
        |||

QY      181  STYRVSVLTIVLHQMNGKEKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
        |||
DB      418  STYRVSVLTIVLHQMNGKEKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 477
        |||

QY      241  LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
        |||
DB      478  LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 537
        |||

QY      301  QOQNVFSCSVMEALAHNYQORSLSLSPGK 330
        |||
DB      538  QOQNVFSCSVMEALAHNYQORSLSLSPGK 567
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RESULT 11
US-09-746-359A-53
; Sequence 53, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenteng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jasper, Stephen R.
; APPLICANT: Chandrasekhar, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-746-359A-53

Query Match          98.0%; Score 1729; DB 4; Length 571;
Best Local Similarity 97.9%; Pred. No. 6.1e-157;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1  ASTKPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNMNSGALTSGVHTFPAVLQSS 60
        |||
DB      242  ASTKPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNMNSGALTSGVHTFPAVLQSS 301
        |||

QY      61  GLYSLSVVTVPSSSLGTQTYICNNHKPSNTKVDKVEPKSCDKTHPCPCPAPPELLGG 120
        |||
DB      302  GLYSLSVVTVPSSSLGTQTYICNNHKPSNTKVDKVEPKSCDKTHPCPCPAPPELLGG 361
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Qy	121	PSVLFPPKPKDPTLMI	STPEVTCVVVDVSHEDPEVKFMWYDGVENHVKTRPREEOYN	180	
Db	362	PSVLFPPKPKDPTLMI	STRPEVTCVVVDVSHEDPEVKFRMYDGVENNAKTRPREEOYN	421	
Qy	181	STYRVSVTLVLHQQNMNGKEKCKVSNKALPAPI	EKTIISKAKVQPREPOVYTLPPSRDE	240	
Db	422	STYRVSVTLVLHQQNMNGKEKCKVSNKALPAPI	EKTIISKAKGPREPOVYTLPPSRDE	481	
Qy	241	LTKNQVSLTCLVKGYGSPSDIAEWESNQPENNY	KTTTPVLDSVGSFLLYSKLTVDKSRW	300	
Db	482	LTKNQVSLTCLVKGYGSPSDIAEWESNQPENNY	KTTTPVLDSGSFLLYSKLTVDKSRW	541	
Qy	301	QOQNVFSCSVNHEALHNHYOQRSLSLS	SPGK 330		
Db	542	QOQNVFSCSVNHEALHNHYTKSLSLS	SPGK 571		
RESULT 12					
US-09-313-942-9					
; Sequence 9, Application US/09313942					
; Patent No. 6472179					
; GENERAL INFORMATION:					
; APPLICANT: REGENERON PHARMACEUTICALS, INC.					
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING					
; FILE REFERENCE: REG 203-A					
; CURRENT APPLICATION NUMBER: US/09/313,942					
; PRIOR APPLICATION NUMBER: 09/313,942					
; PRIOR FILING DATE: 1999-05-19					
; PRIOR APPLICATION NUMBER: 60/101,858					
; PRIOR FILING DATE: 1998-09-25					
; NUMBER OF SEQ ID NOS: 32					
; SOFTWARE: FastSeq for Windows Version 3.0					
; SEQ ID NO 9					
; LENGTH: 951					
; TYPE: PRT					
; ORGANISM: Homo sapiens					
US-09-313-942-9					
Query Match 98.0%; Score 1729; DB 4; Length 951;					
Best Local Similarity 97.9%; Pred. No. 1.3e-156;					
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0					
Qy	1	ASTGSPSVFPLAPSSKSTSGCTAA	GCIVKQYFPPPYVSNWSGALTSQVHFP	PAVLQSS 60	
Db	622	ASTGSPSVFPLAPSSKSTSGG	TAALGCLVKDYFPEPVYVSNWSGALTSQVHFP	PAVLQSS 681	
Qy	61	GLYSLSVVTWPPSSSLSGTQY	ICNVNHNKPSNTRKVDKVPKSCD	KTHTCPCPAP	ELLG 120
Db	682	GLYSLSVVTWPPSSLSGTQY	ICNVNHNKPSNTRKVDKVPKSCD	KTHTCPCPAP	ELLG 741
Qy	121	PSVLFPPKPKDPTLMI	STRPEVTCVVVDVSHEDPEVKFMWYDGV	ENHVKTRPREEOYN 180	
Db	742	PSVLFPPKPKDPTLMI	STRPEVTCVVVDVSHEDPEVKFMWYDGV	ENHNAKTRPREEOYN 801	
Qy	181	STYRVSVTLVLHQQNMNGKEKCKVSNKALPAPI	EKTIISKAKVQPREPOVYTLPPSRDE	240	
Db	802	STYRVSVTLVLHQQNMNGKEKCKVSNKALPAPI	EKTIISKAKGPREPOVYTLPPSRDE	861	
Qy	241	LTKNQVSLTCLVKGYGSPSDIAEWESNQPENNY	KTTTPVLDSVGSFLLYSKLTVDKSRW	300	
Db	862	LTKNQVSLTCLVKGYGSPSDIAEWESNQPENNY	KTTTPVLDSGSFLLYSKLTVDKSRW	921	
Qy	301	QOQNVFSCSVNHEALHNHYOQRSLSLS	SPGK 330		
Db	922	QOQNVFSCSVNHEALHNHYTKSLSLS	SPGK 951		
RESULT 13					
US-09-289-942A-7					
; Sequence 7, Application US/09289942A					

```

? Patent No. 6482928
? GENERAL INFORMATION:
? APPLICANT: Pat, Emil F.
? APPLICANT: Klein, Michel H.
? APPLICANT: Chong, Pele
? APPLICANT: Pedyceak, Arthur
? TITLE OF INVENTION: Fab-EPITYPE COMPLEX FROM THE HIV-1 CROSS-NEUTRALIZING
? TITLE OF INVENTION: MONOCLONAL ANTIBODY 2P5
? FILE REFERENCE: 1038-926 MIS:jd
? CURRENT APPLICATION NUMBER: US/09/289,942A
? CURRENT FILING DATE: 1999-04-13
? NUMBER OF SEQ ID NOS: 9
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 7
? LENGTH: 462
? TYPE: PRT
? ORGANISM: Human immunodeficiency virus type 1
? OS-09-289-942A-7

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	Query Match	Similarity	97.8%	Score	1725;	DB 4;	Length	462;
	Best Local	Similarity	97.6%	Pred.	1.1e-156;			
	Matches	322;	Conservative	3;	Mismatches	5;	Indels	0;
QY	1	ASTGSPVFPLPABSSKSTSGCTAALGCLVYDYPPEPVTSWNSGALTSGVHTPAVLQSS	60					
Db	133	ASTGSPVFPLPABSSKSTSGCTAALGCLVYDYPPEPVTSWNSGALTSGVHTPAVLQSS	192					
QY	61	GLVSLSSVTVTPSSSLGTOYIICVNNHKKPSNTKYDKKVEPSCCKHTTCPPCPAPELLGG	120					
Db	193	GLVSLSSVTVTPSSSLGTOYIICVNNHKKPSNTKYDKKVEPSCCKHTTCPPCPAPELLGG	252					
QY	121	PSVFLPFPKPKDITLMISRTPEVTCVAVDVSHEDPEVKFNMYVDSEVHNHYVTKKREEOYN	180					
Db	253	PSVFLPFPKPKDITLMISRTPEVTCVAVDVSHEDPEVKFNMYVDSEVHNHYVTKKREEOYN	312					
QY	181	STYRVSVLTVLHQNMNNGKYEKKYCSNKALPAIEIKTISKAKVQPREPOVYTLPPSHDE	240					
Db	313	STYRVSVLTVLHQDMNLNGKYEKKYCSNKALPAIEIKTISKAKQPREPOVYTLPPSHDE	372					
QY	241	LTKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW	300					
Db	373	LTKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW	432					
QY	301	QCGNVFSCSVWHEALHNHYOORSLSLSPGK	330					
Db	433	QCGNVFSCSVWHEALHNHYOORSLSLSPGK	462					

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RESULT 14
US-09-740-002-27
; Sequence 27, Application US/09740002
; Patent No. 6537809
; GENERAL INFORMATION:
; APPLICANT: BRAMS, PETER
; APPLICANT: MORROW, PHILLIP
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
; TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
; FILE REFERENCE: 037003-0275759
; CURRENT APPLICATION NUMBER: US/09/740,002
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/335,697
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/488,376
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 475
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-740-002-27

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Query Match 97.8%; Score 1725; DB 4; Length 475;  
Best Local Similarity 97.6%; Pred. No. 1.1e-156;  
Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ASTKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPAVLQSS 60  
Db 146 ASTKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPAVLQSS 205  
Qy 61 GLYSLSVVTVPSSSSLGTQTYICNNHKSNTKVDKVEPKSCDKHTHCPCPAPPELLGG 120  
Db 206 GLYSLSVVTVPSSSSLGTQTYICNNHKSNTKVDKVEPKSCDKHTHCPCPAPPELLGG 265  
Qy 121 PSVFLPPPKPDKDTLMSRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEOYN 180  
Db 266 PSVFLPPPKPDKDTLMSRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEOYN 325  
Qy 181 STYRVVSVLTVLHQMNMNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
Db 326 STYRVVSVLTVLHQMNMNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 385  
Qy 241 LTKNOVSLTCLVKGYFSPDIAVWESNQPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW 300  
Db 386 LTKNOVSLTCLVKGYFSPDIAVWESNQPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW 445  
Qy 301 QQGNVFSCSVMEALAHNHYYQKSLSLSPGK 330  
Db 446 QQGNVFSCSVMEALAHNHYYQKSLSLSPGK 475

RESULT 15  
US-08-487-550-4  
; Sequence 4, Application US/08487550  
; Patent No. 613898  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,550  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teekin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-131  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 476 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: Protein  
; US-08-487-550-4

Query Match 97.8%; Score 1725; DB 3; Length 476;  
Best Local Similarity 97.6%; Pred. No. 1.1e-156;

Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ASTKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPAVLQSS 60  
Db 147 ASTKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPAVLQSS 206  
Qy 61 GLYSLSVVTVPSSSSLGTQTYICNNHKSNTKVDKVEPKSCDKHTHCPCPAPPELLGG 120  
Db 207 GLYSLSVVTVPSSSSLGTQTYICNNHKSNTKVDKVEPKSCDKHTHCPCPAPPELLGG 266  
Qy 121 PSVFLPPPKPDKDTLMSRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEOYN 180  
Db 267 PSVFLPPPKPDKDTLMSRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEOYN 326  
Qy 181 STYRVVSVLTVLHQMNMNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
Db 327 STYRVVSVLTVLHQMNMNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386  
Qy 241 LTKNOVSLTCLVKGYFSPDIAVWESNQPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW 300  
Db 387 LTKNOVSLTCLVKGYFSPDIAVWESNQPENNYKTTTPVLDSVGSFFLYSKLTVDKSRW 446  
Qy 301 QQGNVFSCSVMEALAHNHYYQKSLSLSPGK 330  
Db 447 QQGNVFSCSVMEALAHNHYYQKSLSLSPGK 476

Search completed: June 7, 2005, 09:04:00  
Job time: 47.1658 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 08:48:08 ; Search time 24.4421 Seconds  
(without alignments)  
913.271 Million cell updates/sec

Title: US-10-000-439-3

Perfect score: 1260  
Sequence: 1 EPKSCDKTHTCPCPAPEL.....MHEALHNYQKSLSLSPK 232

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1: \*  
2: p1r2: \*  
3: p1r3: \*  
4: p1r4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1225	97.2	330	1 GHU	Ig gamma-1 chain C
2	1219	96.7	374	2 S69339	Ig heavy chain V r
3	1217	96.6	255	4 S31866	Ig gamma-1 chain C
4	1172	93.0	234	2 PT0207	Ig gamma chain C r
5	1138	90.3	377	2 A23511	Ig gamma-3 chain C
6	1136	90.2	377	2 A60764	Ig gamma-3 chain C
7	1123	89.1	289	1 G3HWT1	Ig gamma-3 heavy C
8	1107	87.9	326	1 G2HU	Ig gamma-2 chain C
9	1097	87.1	327	1 G4HU	Ig gamma-4 chain C
10	883	70.1	323	1 GHRB	Ig gamma chain C r
11	868.5	68.9	328	2 I47160	Ig gamma 2b chain
12	868.5	68.9	328	2 I47159	Ig gamma 2a chain
13	865	68.7	277	2 I47162	Ig gamma 4 chain C
14	858	68.1	329	1 G2GP	Ig gamma-2 chain C
15	847.5	67.3	328	2 I47158	Ig gamma 1 chain C
16	840.5	66.7	328	2 I47161	Ig gamma 3 chain C
17	820	65.1	470	2 S22080	Ig heavy chain pre
18	813	64.5	333	2 PS0018	Ig gamma-2b chain
19	812.5	64.5	329	1 G3MSC	Ig gamma-3 chain C
20	811.5	64.4	308	2 C30554	Ig heavy chain C r
21	811.5	64.4	472	2 S31459	Ig gamma-1 chain C
22	801.5	63.6	398	1 G3MSM	Ig gamma-1 chain C
23	794.5	63.1	444	2 PC4436	monoclonal antibod
24	789.5	62.7	324	1 G1MS	Ig gamma-1 chain C
25	784.5	62.3	326	2 PS0017	Ig gamma-1 chain C
26	784.5	62.3	393	1 G1MSM	Ig gamma-1 chain C
27	776.5	61.6	329	2 S00847	Ig gamma-2c chain
28	776	61.6	330	1 G2MSA	Ig gamma-2a chain
29	776	61.6	469	2 S37483	Ig gamma-2a chain

30	772	61.3	335	1 G2MSAB	Ig gamma-2a chain
31	771	61.2	399	1 G2MSAM	Ig gamma-2a chain
32	761	60.4	446	2 S40295	Ig gamma-2a chain
33	751.5	59.6	474	1 G2MS11	Ig gamma-2b chain
34	747.5	59.3	322	2 PS0019	Ig gamma-2a chain
35	746.5	59.2	405	1 G2MSBM	Ig gamma-2b chain
36	735	58.3	327	2 S06311	Ig gamma-2 chain C
37	731.5	58.1	475	2 S01321	Ig gamma-2b chain
38	669	53.1	180	2 I46732	Ig gamma heavy cha
39	549	43.6	249	2 S69340	Ig heavy chain vH1
40	547	43.4	218	2 A36040	Ig heavy chain V-I
41	542	43.0	152	2 S14236	Ig gamma-1 chain C
42	366.5	29.1	572	2 B46529	Ig gamma-1 chain C
43	357	28.3	549	2 S04845	Ig heavy chain pre
44	353	28.0	343	2 S25644	Ig mu chain C regi
45	353	28.0	455	1 MHMS	Ig mu chain C regi

#### ALIGNMENTS

##### RESULT 1

GHU  
Ig gamma-1 chain C region - human  
C/Species: Homo sapiens (man)  
C/Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004  
C/Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146  
R/Elison, J.W.; Berson, B.J.; Hood, L.E.  
Nucleic Acids Res. 10, 4071-4079, 1982  
A/Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.  
A/Reference number: A93433; MUID:82274238; PMID:6287432  
A/Accession: A93433  
A/Molecule type: DNA  
A/Residues: 1-330 <ELU>  
A/Cross-references: UNIPROT: P01857; EMBL: Z17370  
A/Note: This sequence has the Gln(17) allotypic marker, 97-Lys, and the Gln(1) markers, 2 R/Harris, L.J.  
submitted to the EMBL Data Library, October 1992  
A/Reference number: S33904  
A/Accession: S36861  
A/Molecule type: DNA  
A/Residues: 2-330 <HAR>  
A/Cross-references: EMBL: Z17370  
R/Takahashi, N.; Ueda, S.; Obara, M.; Nikaido, T.; Nakai, S.; Honjo, T.  
Cell 29, 671-679, 1982  
A/Title: Structure of human immunoglobulin gamma genes: implications for evolution of a C  
A/Reference number: S33887; MUID:83001943; PMID:6811139  
A/Accession: S33887  
A/Molecule type: DNA  
A/Residues: 88-113; 235-330 <TRK>  
A/Cross-references: EMBL: Z17370  
R/Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.U.; Edelman, C  
Biochemistry 9, 3161-3170, 1970  
A/Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequenc  
A/Reference number: A90563; MUID:71064024; PMID:5489771  
A/Contents: myeloma protein Bu  
A/Accession: B90563  
A/Molecule type: protein  
A/Residues: 1-96, 'R', 98-135 <GUN>  
A/Note: this sequence has the Gln(3) marker, 97-Arg  
R/Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.  
Biochemistry 9, 3171-3181, 1970  
A/Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen  
A/Reference number: A90564; MUID:71064025; PMID:5530842  
A/Contents: Bu  
A/Accession: A90564  
A/Molecule type: protein  
A/Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240, 'H  
A/Note: this sequence has the Gln(100-1) markers, 239-Glu and 241-Met  
H/Oppe-Seyler, H.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976  
A/Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nle),

Igen Primerstruktur.  
A:Reference number: A91668; MUID:77070269; PMID:826475  
A:Contents: myeloma protein Nie  
A:Accession: B91668  
A:Molecule type: protein  
A:Residues: 1-34, 'Q', '36-96, 'K', '98-115, 'Q', '117-197, 'D', '199-238, 'D', '240, 'L', '242-268, 'E', '27  
A:Note: this sequence has the GIm(17) and GIm(1) markers  
R.Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilsechmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
A:Title: Die Primerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOL  
A:Reference number: A91723; MUID:83289131; PMID:6884994  
A:Contents: myeloma protein KOL; disulfide bonds  
A:Accession: A91723  
A:Molecule type: protein  
A:Residues: 1-96, 'R', '98-197, 'D', '199-238, 'E', '240, 'W', '242-266, 'D', '268-271, 'D', '273-330 <SCH  
A:Note: this sequence has the GIm(3) and GIm(non-1) markers  
R.Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid  
A:Reference number: A90565; MUID:71064027; PMID:4923144  
A:Contents: annotation; disulfide bonds  
R.Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob  
endbromide cleavage products, and the disulfide bridges.  
A:Reference number: A91667; MUID:77070267; PMID:1002129  
A:Contents: annotation; disulfide bonds  
C:Genetics:  
A:Gene: GDB: IGHG1  
A:Cross-references: GDB:120085; OMIM:147100  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1, 114/1, 224/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kg  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1d  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM2>  
F:137-206/Domain: immunoglobulin homology <IM3>  
F:243-310/Domain: immunoglobulin homology <IM3>  
F:127-83,144-204,250-308/Disulfide bonds: #status experimental  
F:103/Disulfide bonds: interchain (to light chain) #status experimental  
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:180/Binding site: carbohydrate (Aen) (covalent) #status experimental

Query Match 97.2%; Score 1225; DB 1; Length 330;  
Best Local Similarity 97.0%; Pred. No. 3, 5e-85;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPBLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 99 EPKSCDKHTHTCPCPAPBLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 158  
QY 61 NMVYDGEVHNAVKTTPREBOYNSTRVSVLTVLHONMNGKEYCKVSNKALPAPIEKT 120  
DB 159 NMVYDGEVHNAVKTTPREBOYNSTRVSVLTVLHONMNGKEYCKVSNKALPAPIEKT 218  
QY 121 ISKAVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTP 180  
DB 219 ISKAGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTP 278  
QY 161 PVLDSVGSFELYSKLTVDKSRWQOGNVFSCVMEHAIHNYTKSLSPGK 232  
DB 279 PVLDSVGSFELYSKLTVDKSRWQOGNVFSCVMEHAIHNYTKSLSPGK 330

RESULT 2  
S69339  
Ig heavy chain V region precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000  
C:Accession: S69339; S72664  
R.Khamlich, A.A.; Auconturier, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995

A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A:Reference number: S69339; MUID:95262687; PMID:7744049  
A:Accession: S69339  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-374 <KHA>  
A:Cross-references: EMBL:X81695  
R.Khamlich, A.A.  
submitted to the EMBL Data Library, September 1994  
A:Reference number: S72664  
A:Accession: S72664  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140, 'C', '142-374 <KH2>  
A:Cross-references: EMBL:X81695  
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 96.7%; Score 1219; DB 2; Length 374;  
Best Local Similarity 96.1%; Pred. No. 1, 2e-84;  
Matches 223; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPBLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 143 EPKSCDKHTHTCPCPAPBLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 202  
QY 61 NMVYDGEVHNAVKTTPREBOYNSTRVSVLTVLHONMNGKEYCKVSNKALPAPIEKT 120  
DB 203 NMVYDGEVHNAVKTTPREBOYNSTRVSVLTVLHONMNGKEYCKVSNKALPAPIEKT 262  
QY 121 ISKAVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTP 180  
DB 263 ISKAGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTP 322  
QY 181 PVLDSVGSFELYSKLTVDKSRWQOGNVFSCVMEHAIHNYTKSLSPGK 232  
DB 323 PVLDSVGSFELYSKLTVDKSRWQOGNVFSCVMEHAIHNYTKSLSPGK 374

RESULT 3  
S31866  
Ig gamma-1 chain C region - synthetic  
C:Species: synthetic  
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli  
C:Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000  
C:Accession: S31866  
R.Filipula, D.  
submitted to the EMBL Data Library, February 1993  
A:Description: Screening method for protein-protein interactions of cloned gene products.  
A:Reference number: S31866  
A:Accession: S31866  
A:Molecule type: mRNA  
A:Residues: 1-255 <FIL>  
A:Cross-references: EMBL:X70421; NID:g33068; PID:CAA49866.1; PID:g33069  
C:Keywords: immunoglobulin  
F:1-22/Region: Escherichia coli outer membrane protein A precursor  
F:23-255/Region: human Ig gamma-1 chain C region

Query Match 96.6%; Score 1217; DB 4; Length 255;  
Best Local Similarity 96.6%; Pred. No. 1e-84;  
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPBLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 24 EPKSCDKHTHTCPCPAPBLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 83  
QY 61 NMVYDGEVHNAVKTTPREBOYNSTRVSVLTVLHONMNGKEYCKVSNKALPAPIEKT 120  
DB 84 NMVYDGEVHNAVKTTPREBOYNSTRVSVLTVLHONMNGKEYCKVSNKALPAPIEKT 143  
QY 121 ISKAVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTP 180  
DB 144 ISKAGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTP 203



A:Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication  
 A:Reference number: A92219; MUID:77118561; PMID:402353  
 A:Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein W  
 A:Accession: A92219  
 A:Molecule type: protein  
 A:Residues: 12-97 <MIC>  
 A:Note: the hinge region in gamma-3 chains is about four times as long as in other gamma  
 idue segment (12-28)  
 A:Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter  
 R:Wolfsenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.  
 Biochem. Biophys. Res. Commun. 71, 907-914, 1976  
 A:Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the  
 A:Reference number: A90199; MUID:77021516; PMID:823945  
 A:Contents: heavy chain disease protein ZUC, partial sequence corresponding to residues  
 A:Accession: A90199  
 A:Molecule type: protein  
 A:Residues: 59-125, 'E', 128-226, 228-289 <NOL>  
 A:Note: this protein lacks most of the V region, all of the CH1 region, and part of the  
 R:Alexander, A.; Steimer, M.; Barltan, D.; Frangione, B.; Franklin, E.C.; Hood, L.;  
 Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982  
 A:Title: gamma heavy chain disease in man: CDNA sequence supports partial gene deletion  
 A:Reference number: A93915; MUID:82247835; PMID:808505  
 A:Contents: heavy chain disease protein Omm  
 A:Accession: A93915  
 A:Molecule type: mRNA  
 A:Residues: 12-70, 72-114, 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-157  
 A:Note: a carboxyl-terminal lys is removed posttranslationally  
 A:Note: this sequence may represent an allelic form or another gamma chain subclass  
 A:Comment: The heavy chain disease protein Wis is shown.  
 C:Genetics:  
 A:Gene: GDB:IGHG3  
 A:Cross-references: GDB:119339; OMIM:147120  
 A:Map position: 14q32.33-14q32.33  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: duplication; glycoprotein; immunoglobulin; pyroglyutamic acid  
 F:203-270/Domain: immunoglobulin homology <IMM>  
 F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental  
 F:6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 Query Match 89.1%; Score 1123; DB 1; Length 289;  
 Best Local Similarity 88.3%; Pred. No. 1.5e-77;  
 Matches 204; Conservative 14; Mismatches 13; Indels 0; Gaps 0;  
 Qy 1 EPKCDKHTHTCPGAPRLGSPVFLPPPKKDTLMTSRTEVYCVVVDVSHEDPEYKF 60  
 Db 59 EPKCDTTPPCPCAPRLGSPVFLPPPKKDTLMTSRTEVYCVVVDVSHEDPEYQF 118  
 Qy 61 NWYDGVENVHVKTPREEQYNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120  
 Db 119 KMYDGVQVHNAKTPREEQPNSTYRVVSVLTVLHQNMDGKEYCKVSNKALPAPIEKT 178  
 Qy 121 ISKAVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFPSPDIADVWESNGQPENNYKTP 180  
 Db 179 ISKTGQPREPOVYTLPPSRDEMTKNQVSLTCLVKGFPSPDIADVWESNGQPENNYKTP 238  
 Qy 181 PVLDSVGFELYSKLTVDKSRWQGNVFSCTMHMALNHNQORSLSPG 231  
 Db 239 PVLDSGFFELYSKLTVDKSRWQGNVFSCTMHMALNHNQORSLSPG 289  
 RESULT 8  
 G2HU  
 19 gamma-2 chain C region - human  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #ext\_change 09-Jul-2004  
 C:Accession: A93906; A92809; A90752; A93132; A02148  
 R:Ellison, J.; Hood, L.  
 Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982  
 A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con  
 A:Reference number: A93906; MUID:82197621; PMID:6804948  
 A:Accession: A93906  
 A:Molecule type: DNA  
 A:Residues: 1-326 <ELL>

A:Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:932759; PIDN:CA858438.1; P1  
 A:Note: Lys-326 is probably removed posttranslationally  
 R:Wang, A.C.; Tung, E.; Fudenberg, H.H.  
 J. Immunol. 125, 1048-1054, 1980  
 A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and fi  
 A:Reference number: A92809; MUID:81007873; PMID:6774012  
 A:Contents: myeloma protein T11  
 A:Accession: A92809  
 A:Molecule type: protein  
 A:Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <MAN>  
 A:Note: Trp-156 is at or near the complement-binding site  
 R:Connell, G.E.; Parr, D.M.; Hofmann, T.  
 Can. J. Biochem. 57, 758-767, 1979  
 A:Title: The amino acid sequences of the three heavy chain constant region domains of a  
 A:Reference number: A90752; MUID:80001357; PMID:113060  
 A:Contents: myeloma protein Zie  
 A:Accession: A90752  
 A:Molecule type: protein  
 A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-;  
 A:Note: this sequence has since been revised  
 R:Hofmann, T.; Parr, D.M.  
 Mol. Immunol. 16, 923-925, 1979  
 A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin G;  
 A:Reference number: A93132; MUID:80114419; PMID:118920  
 A:Contents: Zie  
 A:Accession: A93132  
 A:Molecule type: protein  
 A:Residues: 238-275 <HOF>  
 R:Hofmann, T.; Parr, D.M.  
 submitted to the Aclae, March 1980  
 A:Reference number: A94591  
 A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268  
 A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic  
 ned  
 R:Milstein, C.; Frangione, B.  
 Biochem. J. 121, 217-225, 1971  
 A:Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.  
 A:Reference number: A90253; MUID:72033500; PMID:4949472  
 A:Contents: annotation; myeloma protein Sa, disulfide bonds  
 R:Frangione, B.; Milstein, C.; Pink, J.R.L.  
 Nature 221, 145-148, 1969  
 A:Title: Structural studies of immunoglobulin G.  
 A:Reference number: A93157; MUID:69064124; PMID:5782707  
 A:Contents: annotation; Sa, disulfide bonds  
 A:Gene: GDB:IGHG2  
 C:Genetics:  
 A:Cross-references: GDB:119338; OMIM:147110  
 A:Map position: 14q32.33-14q32.33  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)  
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lat  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
 F:20-85/Domain: immunoglobulin homology <IM1>  
 F:133-202/Domain: immunoglobulin homology <IM2>  
 F:239-306/Domain: immunoglobulin homology <IM3>  
 F:14/Disulfide bonds: interchain (to light chain) #status experimental  
 F:27-83,140-200,246-304/Disulfide bonds: #status experimental  
 F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
 F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 87.9%; Score 1107; DB 1; Length 326;  
 Best Local Similarity 88.4%; Pred. No. 2.8e-76;  
 Matches 205; Conservative 12; Mismatches 11; Indels 4; Gaps 2;  
 Qy 1 EPKCDKHTHTCPGAPRLGSPVFLPPPKKDTLMTSRTEVYCVVVDVSHEDPEYKF 60  
 Db 99 ERKCVF---CPGCAFP-VAGSPVFLPPPKKDTLMTSRTEVYCVVVDVSHEDPEYQF 154  
 Qy 61 NWYDGVENVHVKTPREEQYNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120  
 Db 155 NWYDGVENVHNAKTPREEQPNSTYRVVSVLTVLHQNMDGKEYCKVSNKALPAPIEKT 214  
 Qy 121 ISKAVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFPSPDIADVWESNGQPENNYKTP 180

Db 215 ISKRGQREPOVYTLPPSRREMTKNQVSLTCLVGFPSDIAVEMSGOPENNYKTTTP 274  
 Oy 181 PVLDSVGSFPLYSKLTVDKSRMQGNVSCSVMEALHNHYOQRSLISLSPGK 232  
 Db 275 PVLDSVGSFPLYSKLTVDKSRMQGNVSCSVMEALHNHYOQRSLISLSPGK 326

## RESULT 9

G4HU

Ig gamma-4 chain C region - human

C/Species: Homo sapiens (man)

C/Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 09-Jul-2004

C/Accession: A90933; A90249; A02150

R/Elision: J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A/Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A/Reference number: A90933; MUID:83157104; PMID:6299662

A/Accession: A90933

A/Molecule type: DNA

A/Residues: 1-327 &lt;ELH&gt;

A/Cross-references: UNIPROT:P01861

A/Note: the sequence was determined from the germ-line gene

R/Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A/Title: Human immunoglobulin subclases. Partial amino acid sequence of the constant

A/Reference number: A90249; MUID:70207560; PMID:4192699

A/Accession: A90249

A/Molecule type: protein

A/Residues: 1-30; 81-326 &lt;PIN&gt;

C/Genetics:

A/Accession: A90245

A/Residues: 132-143, 'E', 145-161 &lt;FRU&gt;

R/Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.

in Gamma Globulins; Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell,

A/Reference number: A94416

A/Accession: A94416

A/Molecule type: protein

A/Residues: 129-131; 155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D', 202-217, 'E', 219-232, 'Q',

A/Note: this has the e15 allotypic marker, 185-A1a

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)

chain disulfide bonds. In some cases, such as Iga and IgM, the subunits associate into 1a

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-82/Domain: immunoglobulin homology &lt;IM1&gt;

F:20-85/Domain: immunoglobulin homology &lt;IM1&gt;

F:99-110/Region: hinge

F:134-203/Domain: immunoglobulin homology &lt;IM2&gt;

F:240-307/Domain: immunoglobulin homology &lt;IM3&gt;

F:14/Distal disulfide bonds: interchain (to light chain) #status experimental

F:27-83, 141-201, 247-305/Distal disulfide bonds: #status predicted

F:106, 109/Distal disulfide bonds: interchain (to heavy chain) #status experimental

F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 87.1%; Score 1097; DB 1; Length 327;

Matches 201; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Oy 11 CPPCAPBELLGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNYYVDGVEVH 70  
 Db 106 CPSCAPBELLGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNYYVDGVEVH 165  
 Oy 71 NKTTPREQVNSTRVVSVLTVLHONMNGKVEYCKVSKNKLPAPIETKISKAKQOPRE 130  
 Db 166 NAKTPREQVNSTRVVSVLTVLHONMNGKVEYCKVSKNKLPAPIETKISKAKQOPRE 225  
 Oy 131 PQVYTLPSRDLTKNQVSLTCLVKGFPYSDIAVEMSGOPENNYKTTTPVLDVSGSFF 190  
 Db 226 PQVYTLPSRDLTKNQVSLTCLVKGFPYSDIAVEMSGOPENNYKTTTPVLDVSGSFF 285  
 Oy 191 LYSKLTVDKSRMQGNVSCSVMEALHNHYOQRSLISLSPGK 232  
 Db 286 LYSKLTVDKSRMQGNVSCSVMEALHNHYOQRSLISLSPGK 327

## RESULT 10

GHRB

Ig gamma chain C region - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 24-Apr-1984 #sequence\_revision 15-Nov-1984 #text\_change 09-Jul-2004  
 C/Accession: A91749; A90290; A93928; A90245; A94416; A02161  
 R/Bernstein, K.E.; Alexander, C.B.; Mage, R.G.  
 Immunogenetics 18, 387-397, 1983  
 A/Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-1 haplotype

A/Reference number: A91749; MUID:84030930; PMID:6313520

A/Accession: A91749

A/Molecule type: mRNA

A/Residues: 1-323 &lt;BER&gt;

A/Cross-references: UNIPROT:P01870

A/Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr

R/Piracy, D.M.; Mole, L.E.

Biochem. J. 151, 337-349, 1975

A/Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglob

A/Reference number: A90290; MUID:76135469; PMID:1243651

A/Accession: A90290

A/Molecule type: protein

A/Residues: 1-47, 'E', 49-71, 'PV', 72-128 &lt;PRA&gt;

R/Martens, C.L.; Moore, K.W.; Steimetz, M.; Hood, L.; Knight, K.L.

Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982

A/Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain

A/Reference number: A93928; MUID:83299917; PMID:6193512

A/Accession: A93928

A/Molecule type: mRNA

A/Residues: 88-103, 'W', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 &lt;MAR&gt;

A/Cross-references: GB:M6426; NID:G16511; PIDN:AA31289.1; PID:G165112

A/Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker

R/Fruehr, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.

Biochem. J. 116, 249-259, 1970

A/Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin (

A/Reference number: A90245; MUID:70110015; PMID:5461106

A/Accession: A90245

A/Molecule type: protein

A/Residues: 132-143, 'E', 145-161 &lt;FRU&gt;

R/Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.

in Gamma Globulins; Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell,

A/Reference number: A94416

A/Accession: A94416

A/Molecule type: protein

A/Residues: 129-131; 155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D', 202-217, 'E', 219-232, 'Q',

A/Note: this has the e15 allotypic marker, 185-A1a

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)

chain disulfide bonds. In some cases, such as Iga and IgM, the subunits associate into 1a

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-82/Domain: immunoglobulin homology &lt;IM1&gt;

F:130-199/Domain: immunoglobulin homology &lt;IM2&gt;

F:236-303/Domain: immunoglobulin homology &lt;IM3&gt;

F:173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 70.1%; Score 883; DB 1; Length 323;

Matches 160; Conservative 34; Mismatches 38; Indels 16; Gaps 2;

Oy 1 BPKSCDKTH-----TC-PPCAPBELLGSPVFLPPPKKDTLMISRTPEV 44  
 Db 76 QPVTGNVAHPATNTKVDKTVAPSTCKPTCPBELLGSPVFLPPPKKDTLMISRTPEV 135  
 Oy 45 TCVVVDVSHEDPEVKFNYYVDGVEVHNYKTRREQVNSTRVVSVLTVLHONMNGKVEY 104  
 Db 136 TCVVVDVSHEDPEVKFNYYVDGVEVHNYKTRREQVNSTRVVSVLTVLHONMNGKVEY 195  
 Oy 105 KCKVSKNKLPAPIETKISKAKQOPREPOVYTLPPSRDELTKNQVSLTCLVKGFPYSDIAV 164  
 Db 196 KCKVSKNKLPAPIETKISKAKQOPREPOVYTLPPSRDELTKNQVSLTCLVKGFPYSDIAV 255  
 Oy 165 EWMESGOPENNYKTTTPVLDVSGSFFLYSKLTVDKSRMQGNVSCSVMEALHNHYOQR 224  
 Db 256 EWMESGOPENNYKTTTPVLDVSGSFFLYSKLTVDKSRMQGNVSCSVMEALHNHYOQR 315  
 Oy 225 SLISLSPGK 232  
 Db 316 SLISLSPGK 323

```
RESULT 11
147160
Ig gamma 2b chain constant region - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C/Accession: 147160
R/Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A/Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A/Reference number: 147158; MUID:95015845; PMID:7930579
A/Accession: 147160
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-328 <KAC>
A/Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C/Genetics:
C/Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match      68.9%; Score 868.5; DB 2; Length 328;
Best Local Similarity 70.1%; Pred. No. 2.8e-58;
Matches 157; Conservative 32; Mismatches 32; Indels 3; Gaps 2;

Db
11 CPPCAPPELLGGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVH 70
106 CPICPACE-SPGPSVFIFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVH 164
71 NVTKPREQVNSTRYVSVLTFLHONMNGKCYKSNKALPAPIETKISKAKVQPRE 130
165 TAQTRPKREQNSTRYVSVLTFLHONMNGKCYKSNKALPAPIETKISKAKVQPRE 224
131 PQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGQ--PENNYKTTTPVLDSVGS 188
225 PQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGQ--PENNYKTTTPVLDSVGS 224
189 FFLYSKLTVDKSRMOQGVNFGSCVMHEALHNHYQOQSLSLSPGK 232
285 YFLYSKFSVDKASWQGGIFQCAVMHEALHNHYTQKSISLTPGK 328

RESULT 12
147159
Ig gamma 2a chain constant region - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C/Accession: 147159
R/Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A/Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A/Reference number: 147158; MUID:95015845; PMID:7930579
A/Accession: 147159
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-328 <KAC>
A/Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C/Genetics:
C/Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match      68.9%; Score 868.5; DB 2; Length 328;
Best Local Similarity 70.1%; Pred. No. 2.8e-58;
Matches 157; Conservative 32; Mismatches 32; Indels 3; Gaps 2;

Db
11 CPPCAPPELLGGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVH 70
106 CPICPACE-SPGPSVFIFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVH 164
71 NVTKPREQVNSTRYVSVLTFLHONMNGKCYKSNKALPAPIETKISKAKVQPRE 130
165 TAQTRPKREQNSTRYVSVLTFLHONMNGKCYKSNKALPAPIETKISKAKVQPRE 224
131 PQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGQ--PENNYKTTTPVLDSVGS 188
225 PQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGQ--PENNYKTTTPVLDSVGS 224
189 FFLYSKLTVDKSRMOQGVNFGSCVMHEALHNHYQOQSLSLSPGK 232
285 YFLYSKFSVDKASWQGGIFQCAVMHEALHNHYTQKSISLTPGK 328
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Db
165 TAQTRPKREQNSTRYVSVLTFLHONMNGKCYKSNKALPAPIETKISKAKVQPRE 224
Qy
131 PQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGQ--PENNYKTTTPVLDSVGS 188
Db
225 PQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGQ--PENNYKTTTPVLDSVGS 108
Qy
169 FFLYSKLTVDKSRMOQGVNFGSCVMHEALHNHYQOQSLSLSPGK 232
285 YFLYSKFSVDKASWQGGIFQCAVMHEALHNHYTQKSISLTPGK 328

RESULT 13
147162
Ig gamma 4 chain constant region - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C/Accession: 147162
R/Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A/Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A/Reference number: 147158; MUID:95015845; PMID:7930579
A/Accession: 147162
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-277 <KAC>
A/Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
C/Genetics:
C/Superfamily: immunoglobulin C region; immunoglobulin homology
F:82-151/Domain: immunoglobulin homology <IMM>

Query Match      68.7%; Score 865; DB 2; Length 277;
Best Local Similarity 69.0%; Pred. No. 4.1e-58;
Matches 158; Conservative 32; Mismatches 35; Indels 4; Gaps 3;

Db
8 THTCPCPC-APELTG-GSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 65
49 TTKTRPCPCICPACGEGPSAFTFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 108
Qy
66 GVEVHNVTKPREQNSTRYVSVLTFLHONMNGKCYKSNKALPAPIETKISKAK 125
109 GVEVHNVTKPREQNSTRYVSVLTFLHONMNGKCYKSNKALPAPIETKISKAK 168
Qy
126 VQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGQ--PENNYKTTTPVL 183
Db
169 GQTRBPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGQ--PENNYKTTTPVL 228
Qy
184 DSVGSFFLYSKLTVDKSRMOQGVNFGSCVMHEALHNHYQOQSLSLSPGK 232
229 DVDGTYFLYSKLTVDKSRMOQGVNFGSCVMHEALHNHYTQKSISLTPGK 277

RESULT 14
GZGP
Ig gamma-2 chain C region - guinea pig
C/Species: Cavia porcellus (guinea pig)
C/Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 09-Jul-2004
C/Accession: A94553; A90352; A90359; A90384; A90385; A02151
R/Trieckmann, T.M.
submitted to the Aclae, April 1975
A/Reference number: A94553
A/Accession: A94553
A/Molecule type: Protein
A/Residues: 1-3 <TRI>
A/Cross-references: UNIPROT:P01862
R/Birchlein, B.K.; Hussain, Q.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
A/Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am
A/Accession: A90352; MUID:71058471; PMID:5358606
A/Molecule type: Protein
A/Residues: 4-68 <BIR>
R/Turner, K.J.; Cebra, J.J.
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Biochemistry 10, 9-17, 1971  
A>Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Amino acid sequence. A90359; MUID:71058486; PMID:5538616  
A'Accession: A90359  
A'Molecule type: protein  
A'Residuals: 69-133/312-329 <TR>  
R:Tracey, D.E.; Cebra, J.J.  
Biochemistry 13, 4796-4803, 1974  
A>Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies. A90384; MUID:75036072; PMID:4429665  
A'Accession: A90384  
A'Molecule type: protein  
A'Residuals: 134-226 <TRA>  
R:Trischmann, T.M.; Cebra, J.J.  
Biochemistry 13, 4804-4811, 1974  
A>Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies. A90385; MUID:75036073; PMID:4609467  
A'Accession: A90385  
A'Molecule type: protein  
A'Residuals: 227-311 <TR2>  
R:Oliveira, B.; Lamm, M.E.  
Biochemistry 10, 26-31, 1971  
A>Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin. A90354; MUID:71058474; PMID:4922544  
A'Accession: A90354  
A'Contents: annotation; disulfide bonds  
A'Note: Cys-16 is involved in a heavy-light chain bond  
A'Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds  
C'Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.  
C'Complex: An immunoglobulin heterodimer subunit consists of two identical light (lambda) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.  
C'Superfamily: immunoglobulin C region; immunoglobulin homology  
C'Keywords: duplication; glycoprotein; heterodimer; immunoglobulin  
F:135-204/Domain: immunoglobulin homology <IM1>  
F:241-310/Domain: immunoglobulin homology <IM2>  
F:28-79/Disulfide bonds: #status experimental  
F:142-202/Disulfide bonds: #status experimental  
F:178/Binding site: carbohydrate (Aan) (covalent) #status experimental  
F:248-308/Disulfide bonds: #status experimental

Query Match 68.1%; Score 858; DB 1; Length 329;  
Best Local Similarity 67.4%; Pred. No. 1.7e-57;  
Matches 157; Conservative 28; Mismatches 42; Indels 6; Gaps 2;

QY 1 EKKSCDKHTCPPEPPELLGSPVFLPPPKDITMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 101 ZBPPC---TCPCPEPPELVGSPVFLPPPKDITMISLTPPVTCVVVDVSHEDPEVKF 156  
QY 61 NMVVDGEVHANYTKPREQYNSTYRVSVLTFLHQMNMNGEKYCKVSNKALPAPIEKT 120  
DB 157 TMFVNDKPKVGNMNETKRVVQYNTTPRVESVLPRIQHODMLRGEKCKVSNKALPAPIEKT 216  
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNQGP--ENNYKT 178  
DB 217 ISKTGAPRMPPVYTLPPSRDELTKSKVSVTCLINFPADIHVEWASNRVPSSEKYN 276  
QY 179 TTPVLDVSGSFLLYSKLTLDKSRWQGNVFSQVMEHALHNHYQORSLSISPG 231  
DB 277 TPEIEDADGSFLYSKLTLDKSRWQGNVFSQVMEHALHNHYQORSLSISPG 329

RESULT 15  
147158  
Ig gamma 1 chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: 147158  
R:Kaczkovics, I.; Sun, J.; Butler, J.E.  
J:Immunol. 153, 3565-3573, 1994  
A>Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a B cell clone. A90358; MUID:95015845; PMID:7930579  
A'Accession: 147158  
A>Status: preliminary; translated from GB/EMBL/DBJ

A'Molecule type: mRNA  
A'Residuals: 1-328 <KAC>  
A'Cross-References: EMBL:U03778; NID:G433121; PIDN:AAA52216.1; PID:G433122  
C:Genetics:  
A:Gene: IgG1  
C'Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IM1>

Query Match 67.3%; Score 847.5; DB 2; Length 328;  
Best Local Similarity 69.3%; Pred. No. 1.1e-56;  
Matches 156; Conservative 30; Mismatches 36; Indels 3; Gaps 2;

QY 10 TCPPEPABELLGSPVFLPPPKDITMISRTPEVTCVVVDVSHEDPEVKFNMVVDGEV 69  
DB 105 TCPPEPGE-VAGPSVFLPPPKDITMISQPEVTCVVVDVSKHAQVQSMVVDGEV 163  
QY 70 HNVKTPREEQYNSTYRVSVLTFLHQMNMNGEKYCKVSNKALPAPIEKTISKAKVQPR 129  
DB 164 HTAETRPKEEQYNSTYRVSVLTFLHQMNMNGEKYCKVSNKALPAPIEKTISKAKVQPR 223  
QY 130 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNQGP--ENNKTTPVLDVSG 187  
DB 224 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNQGPPEENYRTTPPOQDVG 283  
QY 188 SFLLYSKLTLDKSRWQGNVFSQVMEHALHNHYQORSLSISPGK 232  
DB 284 TFLYSKLTLDKSRWQGNVFSQVMEHALHNHYQORSLSISPGK 328

Search completed: June 7, 2005, 09:02:35  
Job time: 26.4421 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 08:39:41 ; Search time 114.197 Seconds

(without alignments)  
1040.329 Million cell updates/sec

Title: US-10-000-439-3

Perfect score: 1260

Sequence: 1 EPKSCDKHTPCPPAPPELL.....MHEALHNHYQQRSLSPGK 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1225	97.2	330	1	GCI_HUMAN
2	1225	97.2	465	2	Q6GEX6
3	1225	97.2	466	2	Q6IN78
4	1225	97.2	469	2	Q7Z7P5
5	1225	97.2	470	2	Q6B2A4
6	1225	97.2	470	2	Q7Z5W1
7	1225	97.2	472	2	Q6N089
8	1225	97.2	475	2	Q6GMW7
9	1225	97.2	476	2	Q6GMX1
10	1225	97.2	479	2	Q6EP08
11	1221	96.9	473	2	Q6P055
12	1221	96.9	475	2	Q6M2Q6
13	1221	96.9	480	2	Q6N094
14	1221	96.9	481	2	Q6N097
15	1221	96.9	482	2	Q7Z351
16	1219	96.7	348	2	Q6PYX1
17	1219	96.7	473	2	Q6M2V7
18	1219	96.7	478	2	Q6P181
19	1219	96.7	480	2	Q6P3F1
20	1218	96.7	466	2	Q6N096
21	1214	96.3	475	2	Q6N095
22	1214	96.3	544	2	Q6EP95
23	1196	94.9	487	2	Q6S2L2
24	1138	90.3	354	2	Q6ET12
25	1138	90.3	518	2	Q6N030
26	1134	90.0	521	2	Q6N4Y9
27	1128	89.5	509	1	GC3_HUMAN
28	1123	89.1	590	2	Q6N1F7
29	1107	87.9	326	1	GC2_HUMAN
30	1107	87.9	417	2	Q6N093
31	1104	87.6	464	2	Q6M2U6

32	1102	87.5	465	2	Q6P6C4	Q6P6C4 homo sapien
33	1097	87.1	327	1	GC4_HUMAN	P01861 homo sapien
34	1097	87.1	473	2	Q6P6C3	Q6P6C3 homo sapien
35	1093	86.7	493	2	Q68CN4	Q68CN4 homo sapien
36	1088	86.3	476	2	Q6MZX7	Q6MZX7 homo sapien
37	983	70.1	323	1	GC_RABIT	P01870 oryctolagus
38	877.5	69.6	337	2	Q6EM34	Q6EM34 equus caball
39	858	68.1	329	1	GC2_CAVPO	P01862 cavia porce
40	813	64.5	333	1	GC6_RAT	P20761 rattus norv
41	812.5	64.5	329	1	GC3_MOUSE	P22436 mus musculu
42	812.5	64.5	470	2	Q7TMK1	Q7TMK1 mus musculu
43	801.5	63.6	303	2	Q6KAM2	Q6KAM2 mus musculu
44	801.5	63.6	398	1	GC3M_MOUSE	P03987 mus musculu
45	795.5	63.1	463	2	Q99LC4	Q99LC4 mus musculu

#### ALIGNMENTS

RESULT 1.	ID	GCI_HUMAN	STANDARD;	PRT;	330 AA.
AC	P01857;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	25-OCT-2004 (Rel. 45, Last annotation update)				
DE	Ig gamma-1 chain C region.				
OS	Name=IGHG1;				
GN	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
NC	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=82274238; PubMed=6287432;				
RA	Ellison J.W., Berson B.O., Hood L.E.;				
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene.";				
RL	Nucleic Acids Res. 10:4071-4079(1982).				
RN	[2]				
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).				
RX	MEDLINE=71064024; PubMed=5489771;				
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,				
RT	Waxdal M.J., Edelman G.M.;				
RL	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";				
RN	Biochemistry 9:3161-3170(1970).				
RP	SEQUENCE OF 136-329 (EU).				
RX	MEDLINE=71064025; PubMed=5530842;				
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,				
RT	Edelman G.M.;				
RL	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";				
RN	Biochemistry 9:3171-3181(1970).				
RP	[4]				
RX	SEQUENCE (MYELOMA PROTEIN NIE).				
RA	MEDLINE=77070269; PubMed=826475;				
RT	Ponertingl H., Hilschmann N.;				
RL	"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein N1e). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";				
RN	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).				
RP	[5]				
RX	SEQUENCE (MYELOMA PROTEIN KOL) AND DISULFIDE BONDS.				
RA	MEDLINE=83289331; PubMed=6884994;				
RT	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;				
RL	"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";				
RN	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).				
RP	[6]				
RX	DISULFIDE BONDS.				
RA	MEDLINE=71064027; PubMed=4923144;				

RA Gall W.E., Edelman G.M.:  
 RT "The covalent structure of a human gamma G-immunoglobulin. X.  
 RL Intrachain disulfide bonds.";  
 RL Biochemistry 9:3188-3196(1970).  
 (7)  
 RP DISULFIDE BONDS.  
 RX MEDLINE=77070267; PubMed=1002129;  
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 RT IgG1 immunoglobulin (myeloma protein Nle), I: purification and  
 RT characterization of the protein, the L- and H-chains, the cyanogen  
 RT bromide cleavage products, and the disulfide bridges.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
 (8)  
 RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RX MEDLINE=81208100; PubMed=7236608;  
 RA Deisenhofer J.;  
 RT "Crystallographic refinement and atomic models of a human Fc fragment  
 RT and its complex with fragment B of protein A from Staphylococcus  
 aureus at 2.9- and 2.8-A resolution.";  
 RL Biochemistry 20:2361-2370(1981).  
 CC -I- MISCELLANEOUS: Nle has the GIM(17) allotypic marker, 97-K, and the  
 GIM(1) markers, 239-D and 241-L. KOL and EU sequences have the  
 CC -I- MISCELLANEOUS: Nle also differs in the amidation states of 35,  
 116, 198, 269 and 272.  
 CC -I- MISCELLANEOUS: EU also differs in the amidation states of residues  
 155, 166, 177, 195, 198, 269, and 272 and in the order of residues  
 268-272.  
 CC -I- MISCELLANEOUS: KOL also differs in the amidation states of  
 residues 198, 267 and 272.  
 -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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 CC EMBL; J00228; AAC82527.1; ALT\_INIT.  
 DR PIR; A93433; GHNU.  
 DR PDB; 1A7J; X-ray; H=1-103.  
 DR PDB; 1DSB; X-ray; B/H=1-101.  
 DR PDB; 1DS1; X-ray; H=1-101.  
 DR PDB; 1D6V; X-ray; H=1-101.  
 DR PDB; 1DN2; X-ray; A/B=120-326.  
 DR PDB; 1B4K; X-ray; A/B=106-329.  
 DR PDB; 1FC1; X-ray; A/B=106-329.  
 DR PDB; 1FC2; X-ray; D=106-329.  
 DR PDB; 1FCJ; X-ray; A=121-326.  
 DR PDB; 1H2H; X-ray; H/K=1-330.  
 DR PDB; 1I7Z; X-ray; B/D=1-103.  
 DR PDB; 1IIS; X-ray; A/B=107-330.  
 DR PDB; 1IIX; X-ray; A/B=107-330.  
 DR PDB; 1L6X; X-ray; A=120-326.  
 DR PDB; 1OQX; X-ray; A/B=119-330.  
 DR PDB; 2RCS; X-ray; H=1-103.  
 DR GeneW; HGNC:5525; IGHG1.  
 DR MIM; 147100; -;  
 DR GO; GO:0005624; C:membrane fraction; NAS.  
 DR GO; GO:0003823; F:antigen binding; TAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00047; Ig\_3.  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 KW 3D-structure; Direct protein sequencing; Glycoprotein;  
 KW Immunoglobulin C region; Immunoglobulin domain.  
 FT NON TER 1 98 CH1.  
 FT DOMAIN 1 98 Hinge.  
 FT DOMAIN 99 110

FT	DOMAIN	111	223	
FT	DOMAIN	224	330	CH2.
FT	DISULFID	27	83	CH3.
FT	DISULFID	103	103	Interchain (with light chain).
FT	DISULFID	109	109	Interchain (with heavy chain).
FT	DISULFID	112	112	Interchain (with heavy chain).
FT	DISULFID	144	204	
FT	DISULFID	250	308	
FT	CARBOHYD	180	180	
FT	VARIANT	97	97	
FT	VARIANT	239	239	N-linked (GLCNAC...).
FT	VARIANT	241	241	K->R (in GIM(3) marker).
FT	STRAND	23	24	/FTid=VAR_003886.
FT	STRAND	26	33	D->E (in GIM(non-1) marker).
FT	STRAND	38	38	/FTid=VAR_003887.
FT	STRAND	41	41	L->M (in GIM(non-1) marker).
FT	TURN	42	45	/FTid=VAR_003888.
FT	TURN	48	49	
FT	TURN	50	52	
FT	STRAND	57	58	
FT	STRAND	59	61	
FT	TURN	62	71	
FT	STRAND	73	75	
FT	HELIX	76	78	
FT	TURN	82	87	
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FT	TURN	92	97	
FT	STRAND	102	103	
FT	TURN	122	126	
FT	STRAND	130	134	
FT	HELIX	136	137	
FT	TURN	141	149	
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FT	TURN	163	164	
FT	STRAND	165	167	
FT	STRAND	171	172	
FT	TURN	176	177	
FT	STRAND	179	180	
FT	TURN	183	190	
FT	STRAND	193	197	
FT	HELIX	198	199	
FT	TURN	202	207	
FT	STRAND	209	210	
FT	TURN	215	219	
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FT	HELIX	238	242	
FT	STRAND	245	256	
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FT	TURN	283	284	
FT	STRAND	287	296	
FT	HELIX	297	301	
FT	TURN	302	303	
FT	STRAND	306	311	
FT	TURN	313	314	
FT	HELIX	316	318	
FT	STRAND	319	324	
SO	SEQUENCE	330 AA;	3770EB106C2FA33D CRC64;	

Query Match 97.2%; Score 1225; DB 1; Length 330;  
 Best Local Similarity 97.0%; Pred. No. 1.8e-88;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPPCAPPELLGGPSVFLFPPPKKDTLMTSRTPETVCYVVDVSHEDPEVKF 60  
 DB 99 EPKSCDKHTHTCPPCAPPELLGGPSVFLFPPPKKDTLMTSRTPETVCYVVDVSHEDPEVKF 158

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QY 61 NMYVDGEVHNVKTKPREQYNSTYRVSVLTFLVHONMNGKEYCKVSNKALPAPIEKT 120
DB 159 NMYVDGEVHNAKTKPREQYNSTYRVSVLTFLVHODMNGKEYCKVSNKALPAPIEKT 218
QY 121 ISKAKQPREPQVYTLPPSRDELTKQVSLTCLVKGFPYSDIAVENESGQPENNYKTP 180
DB 219 ISKAKQPREPQVYTLPPSRDELTKQVSLTCLVKGFPYSDIAVENESGQPENNYKTP 278
QY 181 PVLDSVGSFFLTKLTVDSKRWQGVNFGSCVMEHNLHNYOQRLSLSPGK 232
DB 279 PVLDSVGSFFLTKLTVDSKRWQGVNFGSCVMEHNLHNYOQRLSLSPGK 330

RESULT 2
O6GMX6 PRELIMINARY; PRT; 465 AA.
AC O6GMX6;
DT 05-JUL-2004 (TRMBLrel. 27, Created)
DT 05-JUL-2004 (TRMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-cells;
RX MEDLINE=23288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ushed T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.
DB EMBL; BC073766; AAH73766.1; -
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG-cl.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF07654; Cl-set; 3.
DR Pfam: PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS50290; IG_MHC; UNKNOWN_2.
DR Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FD1386E CRC64;

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Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EFKSCDKHTTCCPCAPABELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 234 EFKSCDKHTTCCPCAPABELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 293
QY 61 NMYVDGEVHNVKTKPREQYNSTYRVSVLTFLVHONMNGKEYCKVSNKALPAPIEKT 120
DB 294 NMYVDGEVHNAKTKPREQYNSTYRVSVLTFLVHODMNGKEYCKVSNKALPAPIEKT 353
QY 121 ISKAKQPREPQVYTLPPSRDELTKQVSLTCLVKGFPYSDIAVENESGQPENNYKTP 180
DB 354 ISKAKQPREPQVYTLPPSRDELTKQVSLTCLVKGFPYSDIAVENESGQPENNYKTP 413
QY 181 PVLDSVGSFFLTKLTVDSKRWQGVNFGSCVMEHNLHNYOQRLSLSPGK 232
DB 414 PVLDSVGSFFLTKLTVDSKRWQGVNFGSCVMEHNLHNYOQRLSLSPGK 465

RESULT 3
O6IN78 PRELIMINARY; PRT; 466 AA.
AC O6IN78;
DT 05-JUL-2004 (TRMBLrel. 27, Created)
DT 05-JUL-2004 (TRMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=23288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ushed T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.
DB EMBL; BC072419; AAH72419.1; -
DR HSSP; P01861; IAD0.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG-cl.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.

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Query Match 97.2%; Score 1225; DB 2; Length 465;  
 Best Local Similarity 97.0%; Pred. No. 2.8e-88;

DR PROSITE: PS00290; IG\_MHC; UNKNOWN 2.  
 SQ SEQUENCE 466 AA; 50853 MW; 53EB0BCDEB81076E CRC64;  
 Query Match 97.2%; Score 1225; DB 2; Length 466;  
 Best Local Similarity 97.0%; Pred. No. 2.8e-88;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHHTCPCPAPPELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 |||||  
 DB 235 EPKSCDKTHHTCPCPAPPELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 294  
 |||||  
 QY 61 NMVYDGVENVHNAKTKPREEQVNSTRYVSVLTVLHQNMMNGKEYCKVSNKALPAPIKT 120  
 |||||  
 DB 295 NMVYDGVENVHNAKTKPREEQVNSTRYVSVLTVLHQNMMNGKEYCKVSNKALPAPIKT 354  
 |||||  
 QY 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 180  
 |||||  
 DB 355 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 414  
 |||||  
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEHALHNHYQQRSLSPGK 232  
 |||||  
 DB 415 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEHALHNHYQQRSLSPGK 466

RESULT 4  
 0727P5 PRELIMINARY; PRT; 469 AA.  
 AC 0727P5;  
 DT 01-OCT-2003 (TREMBLrel. 25, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE IGH1 protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Usetin T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
 Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,  
 Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Strausberg R.;  
 RL Submitted (APR-2003) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; BC051328; AAH51328.1; -  
 DR HSSP; P01857; 1HZH.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; CI-set; 3.  
 DR SMART; SMO0406; IGV; 1.

DR PROSITE: PS00835; IG LIKE; 4.  
 SQ SEQUENCE 469 AA; 51395 MW; C8D5B812BAAP795C CRC64;  
 Query Match 97.2%; Score 1225; DB 2; Length 469;  
 Best Local Similarity 97.0%; Pred. No. 2.8e-88;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHHTCPCPAPPELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 |||||  
 DB 238 EPKSCDKTHHTCPCPAPPELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 297  
 |||||  
 QY 61 NMVYDGVENVHNAKTKPREEQVNSTRYVSVLTVLHQNMMNGKEYCKVSNKALPAPIKT 120  
 |||||  
 DB 298 NMVYDGVENVHNAKTKPREEQVNSTRYVSVLTVLHQNMMNGKEYCKVSNKALPAPIKT 357  
 |||||  
 QY 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 180  
 |||||  
 DB 358 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 417  
 |||||  
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEHALHNHYQQRSLSPGK 232  
 |||||  
 DB 418 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEHALHNHYQQRSLSPGK 469

RESULT 5  
 06PJ4 PRELIMINARY; PRT; 470 AA.  
 AC 06PJ4;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Usetin T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
 Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,  
 Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; BC018747; AAH18747.1; -  
 DR HSSP; P01861; IADQ.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR InterPro; IPR003596; IG\_v.

DR Pfam: PF07654; Cl-set: 3.  
DR SMART; SM00409; IG: 2.  
DR SMART; SM00407; IGcl: 3.  
DR SMART; SM00406; IGv: 1.  
DR PROSITE; PS50835; IG LIKE: 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 470 AA; 51715 MW; 7849556A11FD7D9 CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 470;  
Best Local Similarity 97.0%; Pred. No. 2.8e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EFKSCDKHTHTCPCPAPELLGGPSVFLFPKPCKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
DB 239 EFKSCDKHTHTCPCPAPELLGGPSVFLFPKPCKDTLMSRTPEVTCVVVDVSHEDPEVKF 298  
QY 61 NMVYDGEVHNKTKPREQYNSTRYVSVLTVLHQNMMNGKEYCKVSNKKALPAPIEKT 120  
DB 239 NMVYDGEVHNKTKPREQYNSTRYVSVLTVLHQNMMNGKEYCKVSNKKALPAPIEKT 358  
QY 121 ISKAVQPREPQVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVWESNGQPENNYKTP 180  
DB 359 ISKAVQPREPQVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVWESNGQPENNYKTP 418  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEALHNHYOQRLSLSPGK 232  
DB 419 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEALHNHYOQRLSLSPGK 470

## RESULT 6

Q725W1 PRELIMINARY; PRT; 470 AA.

DT 01-OCT-2003 (TRENBLrel. 25, Created)  
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBI\_TaxID=9606;

RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Scheffer C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein W.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loguettano N.A., Peters G.J., Abterson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Gittwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.B.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Splice;  
RA Strausberg R.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC053984; AAH53984.1; -.

DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; Cl-set: 3.  
DR SMART; SM00406; IGv: 1.  
DR PROSITE; PS50835; IG LIKE: 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 470;  
Best Local Similarity 97.0%; Pred. No. 2.8e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EFKSCDKHTHTCPCPAPELLGGPSVFLFPKPCKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
DB 239 EFKSCDKHTHTCPCPAPELLGGPSVFLFPKPCKDTLMSRTPEVTCVVVDVSHEDPEVKF 298  
QY 61 NMVYDGEVHNKTKPREQYNSTRYVSVLTVLHQNMMNGKEYCKVSNKKALPAPIEKT 120  
DB 239 NMVYDGEVHNKTKPREQYNSTRYVSVLTVLHQNMMNGKEYCKVSNKKALPAPIEKT 358  
QY 121 ISKAVQPREPQVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVWESNGQPENNYKTP 180  
DB 359 ISKAVQPREPQVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVWESNGQPENNYKTP 418  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEALHNHYOQRLSLSPGK 232  
DB 419 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMEALHNHYOQRLSLSPGK 470

## RESULT 7

Q6N089 PRELIMINARY; PRT; 472 AA.

AC Q6N089;  
DT 05-JUL-2004 (TRENBLrel. 27, Created)  
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686p15220.  
GN Name=DKFZp686p15220;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBI\_TaxID=9606;

RA Fobio G., Han M., Wiemann S.;  
RA Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640627; CAB45781.1; -.  
DR HSP; P01861; IADQ.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; Cl-set: 3.  
DR SMART; SM00409; IG: 2.  
DR SMART; SM00407; IGcl: 3.  
DR SMART; SM00406; IGv: 1.

DR PROSITE; PS50835; IG LIKE: 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 472;  
Best Local Similarity 97.0%; Pred. No. 2.8e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EFKSCDKHTHTCPCPAPELLGGPSVFLFPKPCKDTLMSRTPEVTCVVVDVSHEDPEVKF 60

Dd		241	EPKSCDKHTCPCCPAPELLGGPSVFLFPPPKDKDTLMISSLRPEVTCTCVVDVSHEDPEVKF	3000
Qy		61	NMWVDDVEVHNKTKRKREQYNSTRVYSLTVLHONMNGKEVKCKRYSNALPAPLEKT	1200
Dd		301	NMWVDDVEVHNATKTRERQYNSTRVYSLTVLHQDLNKGKKCRYSNALPAPIEKT	3600
Qy		121	ISAKAQPREPQQVYTLTPSPRDELITKNQVSLTCLVAGFPSPDIAVWEESNQGPENNYKTPP	1800
Dd		361	ISAKAQPREPQQVYTLTPSPRDELITKNQVSLTCLVAGFPSPDIAVWEESNQGPENNYKTPP	4200
Qy		181	PVLDSVGSEFFLYSKLTVDKSRMQQGNVGSCVMHEBALHHNYQQRSLSPGK	232
Dd		421	PVLDSVGSEFFLYSKLTVDKSRMQQGNVGSCVMHEBALHHNYQQRSLSPGK	472
<hr/>				
RESULT 8				
Q6GMW7	ID	O6GMW7	PRELIMINARY; PRT; 475 AA.	
AC		O6GMW7;		
DT	05-JUL-2004	(TREMBLrel. 27, Created)		
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)		
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)		
DE	Hypotheical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Spleen;			
RA	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Boone T., Max S.I., Wang J., Hsieh F.,			
RA	Hopkins R.F., Jordan H., Moore T., Ma S.I., Wang J., Hsieh F.,			
RA	Diatchenko U., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Sapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,			
RA	Bromstein M.J., Usdin T.B., Toshiyuki S., Cantoni P., Prange C.,			
RA	Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., Mcwan P.J., McKernan K.U., Malek J.A., Gunnarac P.H.,			
RA	Richardson D.K., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,			
RA	Villalón D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schultz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smalov D.E., Scherch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RL	and mouse cDNA sequences."			
RN	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RP	[2]			
RC	SEQUENCE FROM N.A.			
RC	TISSUE=Spleen;			
RA	Strausberg R.;			
RL	Submitted (JUN-2004) to the EMBL/Genbank/DBSJ databaes.			
DR	EMBL: BC073782; AAA73782.1; -.			
DR	InterPro: IPR003599; IG.			
DR	InterPro: IPR007110; IG-like.			
DR	InterPro: IPR003597; IG_1C.			
DR	InterPro: IPR003006; IG_MHC.			
DR	InterPro: IPR003596; IG_V.			
DR	Pfam: pf07654; Cl-sect. 3.			
DR	Pfam: PF00047; Ig_4.			
DR	SMART; SM00409; Ig_2.			
DR	SMART; SM00407; IGC1; 3.			
DR	SMART; SM00406; IGV_1.			
DR	PROSITE: PSS0835; IG_LIKE_4.			
DR	PROSITE: PSS00290; IG_MHC; UNKNOWN_2.			
KW	Hypothetical protein.			
QO	SEQUENCE 475 AA; 51987 MW; 2AIFES5DJ736860F8 CRC64;			

Query Match	Similarity	97.2%	Score	1225;	DB 2;	Length	475;
Best Local	Similarity	97.0%	Pred.	No.	2.8e-88;		
Matches	225;	Conservative	3;	Mismatches	4;	Indels	0;
							Gaps
							0
Qy	1	EPKSCDHTHTCPPCAPPELLGSPVFLPPPKKOTLMSRTEPYTCVVVDVSHEDPEYK	60				
Db	244	EPKSCDHTHTCPPCAPPELLGSPVFLPPPKKOTLMSRTEPYTCVVVDVSHEDPEYK	303				
Qy	61	NMYVDGVEVHNVKTKPREBOYNSYRVVSVLTVAHOMMNGKEYKCKYSNALPAPIEKT	120				
Db	304	NMYVDGVEVHNVKTKPREBOYNSYRVVSVLTVAHOMMNGKEYKCKYSNALPAPIEKT	363				
Qy	121	ISKAQVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAEVWESNGCPENNYKTP	180				
Db	364	ISKAQVOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAEVWESNGCPENNYKTP	423				
Qy	181	PVLDSVGSFPLYSKLTVDKSRMGOGNVFGCSVMHEALHNHYQOQSLSLSPGK	232				
Db	424	PVLDSVGSFPLYSKLTVDKSRMGOGNVFGCSVMHEALHNHYQOQSLSLSPGK	475				
RESULT 9							
06GMX1	1	PRELIMINARY;	PRT;	476	AA.		
ID	06GMX1						
AC	06GMX1						
DT	05-JUL-2004	(TREMBlrel. 27, Created)					
DT	05-JUL-2004	(TREMBlrel. 27, Last sequence update)					
DT	05-JUL-2004	(TREMBlrel. 27, Last annotation update)					
DE		Hypothetical protein.					
OS		Homo sapiens (Human).					
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;					
OC		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX	NCBI_TaxId=9606;						
RN	[1]						
RP		SEQUENCE FROM N.A.					
RC		TISSUE=Spleen;					
RX		MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;					
RA		Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,					
RA		Klausner R.D., Collins F.S., Wagner L., Shamen C.M., Schult G.D.,					
RA		Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,					
RA		Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,					
RA		Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,					
RA		Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,					
RA		Brownstein W.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,					
RA		Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,					
RA		Bosak S.A., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,					
RA		Richards S., Wocley K.C., Hale S., Garcia A.M., Gay L.J., Philyk S.W.,					
RA		Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,					
RA		Hayley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,					
RA		Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,					
RA		Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,					
RA		Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,					
RA		Krzywinski M.I., Skelton U., Smallie D.E., Schermer A., Schein J.E.,					
RA		Jones S.J., Marra M.A.;					
RT		"Generation and initial analysis of more than 15,000 full-length human					
RT		and mouse cDNA sequences."					
RL		Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).					
RN	[2]						
RP		SEQUENCE FROM N.A.					
RC		TISSUE=Spleen;					
RA		Strausberg R.;					
RL		Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.					
DR	EMBL; BC073773; AAH73773.1;						
DR	InterPro; IPR003599; Iq.						
DR	InterPro; IPR007110; Iq-like.						
DR	InterPro; IPR003597; Iq-cl.						

DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C6ZDDE9D CRC64;  
Query Match 97.2%; Score 1225; DB 2; Length 476;  
Best Local Similarity 97.0%; Pred. No. 2.8e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
DB 245 EPKSCDKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 304  
QY 61 NMYVDGVEVHNAKTKRREEQYNSTRYVSVLTYLHQNMNGEKYCKKVSNNKALPAPIEKT 120  
DB 305 NMYVDGVEVHNAKTKRREEQYNSTRYVSVLTYLHQNMNGEKYCKKVSNNKALPAPIEKT 364  
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNQGPENNYKTTTP 180  
DB 365 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNQGPENNYKTTTP 424  
QY 181 PVLDSVGSFFLYSKLTVDKSRMQQGNVFSCSVHREALHNHYOQRSLSISPGK 232  
DB 425 PVLDSVGSFFLYSKLTVDKSRMQQGNVFSCSVHREALHNHYOQRSLSISPGK 476  
RESULT 10  
Q96P08 PRELIMINARY; PRT; 679 AA.  
AC Q96P08;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Factor VII active site mutant immunocjugate.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBI\_TaxID=9606;  
RN NCB1  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;  
HU Z., Garen A.;  
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor  
cells for immunotherapy in mouse models of prostatic cancer."  
Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).  
[2]  
RP SEQUENCE FROM N.A.  
HU Z., Garen A.;  
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF272774; AAK58686.2; -.  
DR HSSP; P08709; 1KLI.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR000152; Asx hydroxyl\_S.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_Like.  
DR InterPro; IPR007110; Ig\_Like.  
DR InterPro; IPR003597; Ig\_C1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR009003; Pept\_Ser\_Cys.  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PF07654; C1\_sec; 2.  
DR Pfam; PF00008; EGF\_1.  
DR Pfam; PF00094; GLA; 1.  
DR Pfam; PF00089; Trypsin; 1.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00407; IgC1; 1.

DR SMART; SM00020; Tryp\_Spc; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS00026; EGF\_3; 1.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00011; GLA\_1; 1.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
DR PROSITE; PS0240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW EGF-like domain; Hydrolase; Protease; Serine protease.  
SQ SEQUENCE 679 AA; 75552 MW; 0B0023AE70A067A1 CRC64;  
Query Match 97.2%; Score 1225; DB 2; Length 679;  
Best Local Similarity 97.0%; Pred. No. 4.3e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
DB 448 EPKSCDKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 507  
QY 61 NMYVDGVEVHNAKTKRREEQYNSTRYVSVLTYLHQNMNGEKYCKKVSNNKALPAPIEKT 120  
DB 508 NMYVDGVEVHNAKTKRREEQYNSTRYVSVLTYLHQNMNGEKYCKKVSNNKALPAPIEKT 567  
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNQGPENNYKTTTP 180  
DB 568 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNQGPENNYKTTTP 627  
QY 181 PVLDSVGSFFLYSKLTVDKSRMQQGNVFSCSVHREALHNHYOQRSLSISPGK 232  
DB 628 PVLDSVGSFFLYSKLTVDKSRMQQGNVFSCSVHREALHNHYOQRSLSISPGK 679  
RESULT 11  
Q96P05 PRELIMINARY; PRT; 473 AA.  
AC Q96P05;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBI\_TaxID=9606;  
RN NCB1  
RP SEQUENCE FROM N.A.  
RP TISSUE=Peripheral Nervous System;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Hsieh F.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.D., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rana S.S., Loquellano N.A., Peters G.J., Abrahamson R.D., Wulliamy S.J.,  
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences."  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]

RP SEQUENCE FROM N.A.  
RC TISSUE=Peripheral Nervous System;  
RA Strausberg R.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC065820; AAH65820.1; -.  
DR HSSP; P01861; IADO.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00407; IG; 2.  
DR SMART; SM00409; IGC1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
DR Hypothetical protein.  
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129857 CRC64;

Query Match 96.9%; Score 1221; DB 2; Length 473;  
Best Local Similarity 96.6%; Pred. No. 5,8e-88;  
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVKF 60  
DB 242 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVKF 301  
QY 61 NMYVDGVEVHANKTPREEQYNSTRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120  
DB 302 NMYVDGVEVHANKTPREEQYNSTRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 361  
QY 121 ISKAVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTP 180  
DB 362 ISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTP 421  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 232  
DB 422 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 473

RESULT 12  
Q6MZ06 PRELIMINARY; PRT; 475 AA.  
AC Q6MZ06;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DR 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
OS Hypothetical protein DKFZp686G11190.  
GN Name=DKFZp686G11190;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human esophagus tumor;  
RA The German Human cDNA Consortium;  
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,  
RA Han M., Wiemann S.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640947; CAE45972.1; -.  
DR HSSP; P01861; IADO.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
DR Hypothetical protein.  
SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;

DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KM Hypothetical protein.  
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match 96.9%; Score 1221; DB 2; Length 475;  
Best Local Similarity 96.6%; Pred. No. 5,8e-88;  
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVKF 60  
DB 244 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVKF 303  
QY 61 NMYVDGVEVHANKTPREEQYNSTRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120  
DB 304 NMYVDGVEVHANKTPREEQYNSTRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 363  
QY 121 ISKAVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTP 180  
DB 364 ISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTP 423  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 232  
DB 424 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 475

RESULT 13  
Q6N094 PRELIMINARY; PRT; 480 AA.  
AC Q6N094;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DR 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
OS Hypothetical protein DKFZp686O01196.  
GN Name=DKFZp686O01196;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human esophagus tumor;  
RA The German Human cDNA Consortium;  
RA Wandt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640622; CAE45776.1; -.  
DR HSSP; P01861; IADO.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
DR Hypothetical protein.  
SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;

Query Match 96.9%; Score 1221; DB 2; Length 480;  
Best Local Similarity 96.6%; Pred. No. 5,9e-88;  
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVKF 60  
DB 249 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVKF 308  
QY 61 NMYVDGVEVHANKTPREEQYNSTRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120  
DB 309 NMYVDGVEVHANKTPREEQYNSTRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 368



QY 121 ISKAVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTP 180  
DB 369 ISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTP 428  
QY 181 PVLDSVGSFELYSKLTVDKSRWQGNVSCSYMHGALHNHYOQRSLSIPGK 232  
DB 429 PVLDSVGSFELYSKLTVDKSRWQGNVSCSYMHGALHNHYOQRSLSIPGK 480

## RESULT 14

Q6N097 PRELIMINARY; PRT; 481 AA.  
AC Q6N097;  
DT 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp668H20196.  
GN Name=DKFZp668H20196;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human esophagus tumor;  
RA The German Human CDNA Consortium;  
RA Mambut R., Heubner D., Mewes H.W., Weil B., Amid C., Oanger A.,  
RA Fobo G., Han M., Wiemann S.,  
RL Submitted (Aug-2003) to the EMBL/Genbank/DBJ databases.  
DR EMBL; BX640619; CAE45773.1; -.  
DR HSSP; P01861; IADQ.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-1-like.  
DR InterPro; IPR003597; IG-1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IG1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 481 AA; 52759 MW; 47220D9E64BDF98B CRC64;

Query Match 96.9%; Score 1221; DB 2; Length 481;  
Best Local Similarity 96.6%; Pred. No. 5.9e-88;  
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPBLILGSPSVFLPPPKKDTLMIISRTPEVTCVVVDVSHEDPEVKF 60  
DB 250 EPKSCDKHTHTCPCPAPBLILGSPSVFLPPPKKDTLMIISRTPEVTCVVVDVSHEDPEVKF 309  
QY 61 NMVYDGEVHNKTKPREQVNSTYRVSVLTVLHONMNGKEYCKVSNKALPAPIEKT 120  
DB 310 NMVYDGEVHNKTKPREQVNSTYRVSVLTVLHONMNGKEYCKVSNKALPAPIEKT 369  
QY 121 ISKAVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTP 180  
DB 370 ISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTP 429  
QY 181 PVLDSVGSFELYSKLTVDKSRWQGNVSCSYMHGALHNHYOQRSLSIPGK 232  
DB 430 PVLDSVGSFELYSKLTVDKSRWQGNVSCSYMHGALHNHYOQRSLSIPGK 481

## RESULT 15

Q72351 PRELIMINARY; PRT; 482 AA.  
AC Q72351;  
DT 01-OCT-2003 (Tremblrel. 25, Created)  
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

DE Hypothetical protein DKFZp668N2209.  
GN Name=DKFZp668N2209;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Oanger A.,  
RA Fobo G., Han M., Wiemann S.,  
RL Submitted (Jun-2003) to the EMBL/Genbank/DBJ databases.  
DR EMBL; BX538118; CAD98026.1; -.  
DR HSSP; P01857; IHDH.  
DR InterPro; IPR007110; IG-1-like.  
DR InterPro; IPR003597; IG-1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 482 AA; 52852 MW; EDA75F1901D1A034 CRC64;

Query Match 96.9%; Score 1221; DB 2; Length 482;  
Best Local Similarity 96.6%; Pred. No. 5.9e-88;  
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPBLILGSPSVFLPPPKKDTLMIISRTPEVTCVVVDVSHEDPEVKF 60  
DB 251 EPKSCDKHTHTCPCPAPBLILGSPSVFLPPPKKDTLMIISRTPEVTCVVVDVSHEDPEVKF 310  
QY 61 NMVYDGEVHNKTKPREQVNSTYRVSVLTVLHONMNGKEYCKVSNKALPAPIEKT 120  
DB 311 NMVYDGEVHNKTKPREQVNSTYRVSVLTVLHONMNGKEYCKVSNKALPAPIEKT 370  
QY 121 ISKAVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTP 180  
DB 371 ISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTP 430  
QY 181 PVLDSVGSFELYSKLTVDKSRWQGNVSCSYMHGALHNHYOQRSLSIPGK 232  
DB 431 PVLDSVGSFELYSKLTVDKSRWQGNVSCSYMHGALHNHYOQRSLSIPGK 482

Search completed: June 7, 2005, 09:01:28  
Job time : 115.197 secs

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CC treating an IGE-mediated biological response, preferably an IGF-mediated  
CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic  
CC dermatitis, severe food allergies, chronic urticaria, angioedema or  
CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,  
CC type-I diabetes mellitus, or multiple sclerosis, and for preventing of,  
CC or symptoms resulting from, a type I hypersensitivity reaction in a  
CC subject receiving immunotherapy. The present sequence is the human IgG1  
CC heavy chain constant region hinge-CH2-CH3 portion  
XX  
SQ Sequence 232 AA;  
Query Match 100.0%; Score 1260; DB 6; Length 232;  
Best Local Similarity 100.0%; Pred. No. 2.9e-91;  
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 BEKSCDKHTHTCPCPAPELLGSPSVFLPPPKRDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
DB 1 BEKSCDKHTHTCPCPAPELLGSPSVFLPPPKRDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
QY 61 NMYVDGVEVHNVKTRPREQYNSTRYVSVLTVLHQMNGEKYCKVSNKALPAPIEKT 120  
DB 61 NMYVDGVEVHNVKTRPREQYNSTRYVSVLTVLHQMNGEKYCKVSNKALPAPIEKT 120  
QY 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTTTP 180  
DB 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTTTP 180  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVMEALHNHYQORSLSLSPGK 232  
DB 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVMEALHNHYQORSLSLSPGK 232  
181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVMEALHNHYQORSLSLSPGK 232  
RESULT 2  
AA019664  
ID AA019664 standard; protein; 330 AA.  
AC AA019664;  
XX  
XX 28-MAR-2003 (first entry)  
DE Human IgG1 heavy chain constant region.  
XX  
XX Human; IgG1; immunoglobulin G; immunotherapy; immune disease;  
KW Fc epsilon receptor; autoimmune disease; constant region; heavy chain;  
KW antiaesthetic; antiallergic; antiinflammatory; dermatological;  
XX antiathrictic; antirheumatic; antidiabetic; neuroprotective.  
OS Homo sapiens.  
XX  
XX WO200288317-A2.  
XX  
XX PD 07-NOV-2002.  
XX  
XX PF 01-MAY-2002; 2002WO-US013527.  
XX  
XX PR 01-MAY-2001; 2001US-00847208.  
XX  
XX PR 24-OCT-2001; 2001US-00000439.  
XX  
XX PA (REGC ) UNIV CALIFORNIA.  
XX  
XX PI Saxon A, Zhang K, Zhu D;  
XX  
XX WPI; 2003-103456/09.  
XX  
XX New fusion molecules comprising polypeptide sequences that bind to IgG  
XX inhibitory receptor and native IGF receptor, useful for treating IGF-  
XX mediated hypersensitivity reactions, e.g. asthma or allergies, or  
XX autoimmune diseases.  
XX  
XX Claim 64; Fig 2; 116pp; English.  
XX  
XX The present invention relates to a fusion molecule comprising a first  
XX polypeptide sequence capable of specific binding to a native IgG

CC inhibitory receptor consisting of an immune receptor tyrosine-based  
CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,  
CC functionally connected to a second polypeptide sequence capable of  
CC specific binding directly or indirectly to a native IGF receptor  
CC (Fc epsilon1). Also provided are nucleotide sequences encoding such a  
CC fusion protein. The fusion molecules and compositions are useful for  
CC creating an IGF-mediated biological response, preferably an IGF-mediated  
CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic  
CC dermatitis, severe food allergies, chronic urticaria, angioedema or  
CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,  
CC type-I diabetes mellitus, or multiple sclerosis, and for preventing of,  
CC or symptoms resulting from, a type I hypersensitivity reaction in a  
CC subject receiving immunotherapy. The present sequence is the human IgG1  
CC heavy chain constant region  
XX  
SQ Sequence 330 AA;  
Query Match 100.0%; Score 1260; DB 6; Length 330;  
Best Local Similarity 100.0%; Pred. No. 4.4e-91;  
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 BEKSCDKHTHTCPCPAPELLGSPSVFLPPPKRDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
DB 99 BEKSCDKHTHTCPCPAPELLGSPSVFLPPPKRDTLMSRTPEVTCVVVDVSHEDPEVKF 158  
QY 61 NMYVDGVEVHNVKTRPREQYNSTRYVSVLTVLHQMNGEKYCKVSNKALPAPIEKT 120  
DB 159 NMYVDGVEVHNVKTRPREQYNSTRYVSVLTVLHQMNGEKYCKVSNKALPAPIEKT 218  
QY 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTTTP 180  
DB 219 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTTTP 278  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVMEALHNHYQORSLSLSPGK 232  
DB 279 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVMEALHNHYQORSLSLSPGK 330  
RESULT 3  
AA019668  
ID AA019668 standard; protein; 569 AA.  
AC AA019668;  
XX  
XX 28-MAR-2003 (first entry)  
DE GE2 fusion protein for use in treating immune diseases.  
XX  
XX Human; IGE; immunoglobulin E; immunotherapy; immune disease;  
KW Fc epsilon receptor; autoimmune disease; constant region; heavy chain;  
KW antiaesthetic; antiallergic; antiinflammatory; dermatological; GE2;  
XX antiathrictic; antirheumatic; antidiabetic; neuroprotective;  
XX fusion protein.  
XX  
XX OS Synthetic.  
XX  
XX OS Unidentified.  
XX  
XX PN WO200288317-A2.  
XX  
XX PD 07-NOV-2002.  
XX  
XX PF 01-MAY-2002; 2002WO-US013527.  
XX  
XX PR 01-MAY-2001; 2001US-00847208.  
XX  
XX PR 24-OCT-2001; 2001US-00000439.  
XX  
XX PA (REGC ) UNIV CALIFORNIA.  
XX  
XX PI Saxon A, Zhang K, Zhu D;  
XX  
XX WPI; 2003-103456/09.  
XX  
XX New fusion molecules comprising polypeptide sequences that bind to IgG

PT inhibitory receptor and native IgE receptor, useful for treating IgE-mediated hypersensitivity reactions, e.g. asthma or allergies, or autoimmune diseases.

PS Claim 35; Fig 7; 116pp; English.

CC The present invention relates to a fusion molecule comprising a first  
CC polypeptide sequence capable of specific binding to a native IgE  
CC inhibitory receptor consisting of an immune receptor tyrosine-based  
CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,  
CC functionally connected to a second polypeptide sequence capable of  
CC specific binding directly or indirectly to a native IgE receptor  
CC (Fcεpsilon1). Also provided are nucleotide sequences encoding such a  
CC fusion protein. The fusion molecules and compositions are useful for  
CC treating an IgE-mediated biological response, preferably an IgE-mediated  
CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic  
CC dermatitis, severe food allergies, chronic urticaria, angioedema or  
CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,  
CC type-1 diabetes mellitus, or multiple sclerosis, and for preventing of,  
CC or symptoms resulting from, a type I hypersensitivity reaction in a  
CC subject receiving immunotherapy. The present sequence is a gammaHinge-  
CC CHgamma2-CHgamma3-(Gly4Ser)3-Chepsilon2-Chepsilon3-Chepsilon3 fusion  
CC protein (designated GE2) of the invention

XX Sequence 569 AA;

Query Match 100.0%; Score 1260; DB 6; Length 569;

Best Local Similarity 100.0%; Pred. No. 8.5e-91; Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLPPPKKDTLMTSRTEPVTCVVVDVSHEDPEVKF 60  
DB 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLPPPKKDTLMTSRTEPVTCVVVDVSHEDPEVKF 60  
QY 61 NMVYDGEVHANKTPREBQVNSTYRVSVLTVLHQDNMNGKEKKCKVSNKALPAPIETKT 120  
DB 61 NMVYDGEVHANKTPREBQVNSTYRVSVLTVLHQDNMNGKEKKCKVSNKALPAPIETKT 120  
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 180  
DB 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 180  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQOGNVPSCSYVMEALAHNHYOQRLSLSPGK 232  
DB 181 PVLDSVGSFFLYSKLTVDKSRWQOGNVPSCSYVMEALAHNHYOQRLSLSPGK 232

RESULT 4

AAW26232  
ID AAW26232 standard; protein; 232 AA.

AC AAW26232;

DT 16-MAR-1998 (first entry)

DE Human IgG1 hinge/Fc region.

KW Fusion protein; hydrophilic spacer; recombinant; expression system;  
KW carboxypeptidase; IgG1; immunoglobulin; hinge region; Fc.

XX Homo sapiens.

XX WO9728272-A1.

XX 07-AUG-1997.

XX 31-JAN-1997; 97WO-US001470.

XX 31-JAN-1996; 96US-00595043.

XX (TECH-) TECHNOLOGENE INC.

XX Sgarlato CD;

XX WPI; 1997-402624/37.  
DR N-PSDB; AAT80158.

PT Recombinant protein expression system for fusion protein production -  
PT useful for high quantity production of authentic recombinant proteins.

PS Example 3; Page 133-134; 194pp; English.

CC A novel recombinant vector has been developed which comprises a  
CC nucleotide sequence encoding a fusion protein. The fusion protein  
CC comprises three domains joined together in order, from N-terminus to C-  
CC terminus, of a first domain comprising a protein of interest, a second  
CC domain comprising a hydrophilic spacer and an affinity domain, each  
CC domain comprising amino acid residues. The present sequence represents  
CC the hinge/Fc region of human IgG1, used in example 3 of the present  
CC invention. The recombinant vector is used for the production of authentic  
CC recombinant proteins of interest. The method of the invention is useful  
CC for the expression of fusion proteins capable of isolation by affinity  
CC chromatography in pro- or eukaryotic cells. This method allows for the  
CC efficient cleavage and generation of authentic proteins of interest that  
CC do not contain extraneous (i.e. non-naturally occurring) amino acids

XX Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 2; Length 232;

Best Local Similarity 97.0%; Pred. No. 1.7e-88; Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLPPPKKDTLMTSRTEPVTCVVVDVSHEDPEVKF 60  
DB 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLPPPKKDTLMTSRTEPVTCVVVDVSHEDPEVKF 60  
QY 61 NMVYDGEVHANKTPREBQVNSTYRVSVLTVLHQDNMNGKEKKCKVSNKALPAPIETKT 120  
DB 61 NMVYDGEVHANKTPREBQVNSTYRVSVLTVLHQDNMNGKEKKCKVSNKALPAPIETKT 120  
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 180  
DB 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 180  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQOGNVPSCSYVMEALAHNHYOQRLSLSPGK 232  
DB 181 PVLDSVGSFFLYSKLTVDKSRWQOGNVPSCSYVMEALAHNHYOQRLSLSPGK 232

RESULT 5

AAB28690  
ID AAB28690 standard; protein; 232 AA.

AC AAB28690;

DT 14-FEB-2001 (first entry)

DE Human IgGammal hinge, CH2 and CH3 regions.

KW Human; ACP-1; type II transmembrane protein; cytosolic; antiviral;  
KW antinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV;  
KW human immunodeficiency virus; apoptosis; proliferative disorder; cancer;  
KW hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;  
KW transplant rejection; cardiovascular disease; arteriosclerosis;

XX IgGammal.

XX Homo sapiens.

XX WO200063253-A1.

XX 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US008004.

XX 16-APR-1999; 99US-00293245.

XX

PA (AMGE-) AMGEN INC.  
XX Hau H, Meng S;  
XX WPI; 2000-665240/64.  
XX Fusion protein of AGP-1 protein and an Fc region, used to treat  
PT proliferative disorders, immune disorders, and virally-induced disorders.  
XX  
XX Claim 2; Fig 1; 93pp; English.  
XX  
XX The present sequence was used in the production of AGP-1 fusion proteins.  
CC AGP-1 is a type II transmembrane protein. The fusion proteins comprise an  
CC Fc immunoglobulin region fused to the N-terminal portion of the AGP-1  
CC protein. The fusion proteins can be used to induce apoptosis in a tissue,  
CC and to treat proliferative disorders, immune disorders, or virally-  
CC induced disorders. The proliferative disorders include cancers, such as  
CC breast, prostate, lung or colon cancer. The viral infections include  
CC hepatitis, and acquired immunodeficiency syndrome (AIDS), and the immune  
CC disorders may be autoimmune disorders or transplant rejection.  
CC Cardiovascular diseases such as arteriosclerosis may also be treated. The  
CC AGP-1 containing fusion proteins have increased biological activity  
CC compared to the soluble AGP-1 proteins used in prior art therapies  
XX

## SQ Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 3; Length 232;  
Best Local Similarity 97.0%; Pred. No. 1.7e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPELLGGPSVFLPPPKKDTLMTSRPEVTCVVVDVSHEDPEVKF 60  
DB 1 EPKSCDKHTHTCPCPAPELLGGPSVFLPPPKKDTLMTSRPEVTCVVVDVSHEDPEVKF 60  
QY 61 NMVYDGVGVHNAKTKPREQYNSTYRVVSVLTVLHQDNMNGEKYCKVSNKALPAPIEKT 120  
DB 61 NMVYDGVGVHNAKTKPREQYNSTYRVVSVLTVLHQDNMNGEKYCKVSNKALPAPIEKT 120  
QY 121 ISKAVQPREPOVYTLPPSRDELITKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTT 180  
DB 121 ISKAVQPREPOVYTLPPSRDELITKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTT 180  
QY 181 PVLDSVGSFPLYSKLTVDKSRWQGQNVFSCVMEHALNHNHYQKSLSPGK 232  
DB 181 PVLDSVGSFPLYSKLTVDKSRWQGQNVFSCVMEHALNHNHYQKSLSPGK 232

## RESULT 6

AAB80897 standard; protein; 232 AA.

XX AAB80897;  
XX  
XX 31-MAY-2001 (first entry)  
XX  
XX Human IgGgamma1 hinge, CH2 and CH3 regions.  
XX  
XX Human; IgGgamma1; anticancer; Antimetastatic; Osteogenic;  
XX  
XX lytic bone disease; multiple myeloma; immunoglobulin;  
XX  
XX osteoclast bone metastasis; OPG; osteoprotegerin;  
XX  
XX osteoclast formation inhibition; bone resorption inhibition.  
XX  
XX Homo sapiens.  
XX  
XX MO200117543-A2.  
XX  
XX 15-MAR-2001.  
XX  
XX 18-AUG-2000; 2000WO-US022806.  
XX  
XX 03-SEP-1999; 99US-00389545.  
XX  
XX (AMGE-) AMGEN INC.  
XX  
XX PA

XX Dunstan CR;  
XX WPI; 2001-265936/27.  
XX  
XX Preventing or treating lytic bone diseases, particularly associated with  
PT cancer or metastasis, by administering an osteoprotegerin polypeptide.  
XX  
XX Disclosure; Fig 1; 87pp; English.  
XX

CC The present invention relates to a method for the prevention or treatment  
CC of lytic bone disease or multiple myeloma. Also the method can be used  
CC for preventing metastasis of cancer to bone or osteoclast bone  
CC metastasis. The method comprises administering an OPG (osteoprotegerin)  
CC polypeptide or OPG fusion protein. The OPG proteins (see AAB80898-  
CC AAB80905) can inhibit formation of osteoclasts (and thus bone resorption)  
CC by blocking differentiation from monocytes/macrophage precursors. The  
CC present sequence is the hinge, CH2 and CH3 regions of human IgGgamma1.  
CC This sequence can be used to generate fusion proteins of OPG and  
CC immunoglobulin, for use in the present invention. The generated fusion  
CC proteins can exhibit increased circulating half-lives and slower  
CC clearance times, thereby providing a more sustained activity  
XX

## SQ Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 4; Length 232;  
Best Local Similarity 97.0%; Pred. No. 1.7e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPELLGGPSVFLPPPKKDTLMTSRPEVTCVVVDVSHEDPEVKF 60  
DB 1 EPKSCDKHTHTCPCPAPELLGGPSVFLPPPKKDTLMTSRPEVTCVVVDVSHEDPEVKF 60  
QY 61 NMVYDGVGVHNAKTKPREQYNSTYRVVSVLTVLHQDNMNGEKYCKVSNKALPAPIEKT 120  
DB 61 NMVYDGVGVHNAKTKPREQYNSTYRVVSVLTVLHQDNMNGEKYCKVSNKALPAPIEKT 120  
QY 121 ISKAVQPREPOVYTLPPSRDELITKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTT 180  
DB 121 ISKAVQPREPOVYTLPPSRDELITKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTT 180  
QY 181 PVLDSVGSFPLYSKLTVDKSRWQGQNVFSCVMEHALNHNHYQKSLSPGK 232  
DB 181 PVLDSVGSFPLYSKLTVDKSRWQGQNVFSCVMEHALNHNHYQKSLSPGK 232

## RESULT 7

AA72915 standard; protein; 232 AA.

XX AA72915;  
XX  
XX 13-JUN-2001 (first entry)  
XX  
XX Human partial IgG1 protein comprising hinge, CH2 and CH3 regions.  
XX  
XX Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;  
XX  
XX therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;  
XX  
XX hypercalcemia; osteopenia; osteonecrosis; rheumatoid arthritis;  
XX  
XX osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;  
XX  
XX periodontal.  
XX  
XX Homo sapiens.  
XX  
XX MO200118203-A1.  
XX  
XX 15-MAR-2001.  
XX  
XX 18-AUG-2000; 2000WO-US022797.  
XX  
XX 03-SEP-1999; 99US-00389782.  
XX  
XX (AMGE-) AMGEN INC.  
XX  
XX PA

XX Dunstan CR, Wooden SK, Mann MB;  
PI  
XX  
DR WPI: 2001-244572/25.  
XX  
XX  
PT Osteoprotegerin-Fc protein fusions useful for treating bone loss caused  
PT by e.g. osteoporosis, Paget's disease and osteomyelitis.  
XX  
XX  
PS Claim 3; Fig 1; 119pp; English.  
XX  
XX The patent discloses fusion protein comprising human osteoprotegerin  
CC (OPG) protein fused by linker to human IgG1 Fc portion. OPG negatively  
CC regulates formation of osteoclasts in vitro and in vivo. It blocks the  
CC differentiation of osteoclasts from monocyte or macrophage precursors and  
CC the reabsorption of bone. The OPG-Fc fusion protein is administered for  
CC the treatment of bone loss resulting from osteoporosis, Paget's disease,  
CC osteomyelitis, hypercalcaemia, osteopenia associated with surgery or  
CC steroid administration, osteonecrosis, bone loss due to rheumatoid  
CC arthritis, periodontal bone loss, osteolytic metastasis and/or prosthetic  
CC loosening. The present sequence is partial human immunoglobulin G (Ig G)  
CC 1 protein comprising the hinge and heavy chain constant regions CH2 and  
CC CH3  
XX  
SQ Sequence 232 AA;  
  
Query Match 97.2%; Score 1225; DB 4; Length 232;  
Best Local Similarity 97.0%; Pred. No. 1.7e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
QY 61 NMYVGVGVHNAKTKRREQVNSTYRVSVLTVLIQDMNMGKEYKCKVSNKALPAPIEKT 120  
DB 61 NMYVGVGVHNAKTKRREQVNSTYRVSVLTVLIQDMNMGKEYKCKVSNKALPAPIEKT 120  
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
DB 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSVMEALHNHYQOQSLSLSPGK 232  
DB 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSVMEALHNHYQOQSLSLSPGK 232  
  
RESULT 8  
AAE15347  
ID AAE15347 standard; protein; 232 AA.  
XX  
AC AAE15347;  
XX  
DT 09-APR-2002 (first entry)  
XX  
DE Human immunoglobulin G (IgG) gamma 1 constant heavy chain hinge region.  
XX  
DE Human: erythropoietin; Epo; haematocrit; anaemia; kidney function; IgG;  
XX cancer; myeloid suppressive therapy; anti-viral drug; immunoglobulin G.  
XX  
OS Homo sapiens.  
XX  
PN WO200181405-A2.  
XX  
PD 01-NOV-2001.  
XX  
XX 19-APR-2001; 2001WO-US012836.  
XX  
XX 21-APR-2000; 2000US-00559001.  
XX  
XX (AMGE-) AMGEN INC.  
XX  
XX Egrle JC, Elliott SG, Browne JK, Sitney KC;  
XX  
XX

DR WPI: 2002-034433/04.  
XX  
XX Increasing and maintaining haematocrit in mammal suffering from anemia,  
XX comprising administering hyperglycosylated analog of erythropoietin less  
PT frequently and at lower molar amount of recombinant human erythropoietin.  
XX  
XX  
PS Example 1; Fig 10; 95pp; English.  
XX  
XX The invention relates to a method for increasing and maintaining  
CC haematocrit in a mammal. The method comprises administering a  
CC hyperglycosylated analogue of erythropoietin (Epo) in a pharmaceutical  
CC composition, less frequently than an equivalent molar amount of and at a  
CC lower molar amount than recombinant human Epo (rHuEpo) to obtain a  
CC comparable target haematocrit. Epo is a glycoprotein hormone necessary  
CC for the maturation of erythroid progenitor cells into erythrocytes. Human  
CC Epo analogue is useful for raising and maintaining haematocrit to a  
CC comparable target haematocrit in a mammal suffering from anaemia  
CC associated with a decline or loss of kidney function, myelosuppressive  
CC therapy comprising chemotherapeutic or anti-viral drugs or associated  
CC with excessive blood loss during surgical procedures, and in cancer  
CC condition. The present sequence is human immunoglobulin G (IgG) gamma 1  
CC constant heavy chain (CH2, CH3) hinge region used to construct Epo  
CC hyperglycosylated analogue fusion protein  
XX  
SQ Sequence 232 AA;  
  
Query Match 97.2%; Score 1225; DB 5; Length 232;  
Best Local Similarity 97.0%; Pred. No. 1.7e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
QY 61 NMYVGVGVHNAKTKRREQVNSTYRVSVLTVLIQDMNMGKEYKCKVSNKALPAPIEKT 120  
DB 61 NMYVGVGVHNAKTKRREQVNSTYRVSVLTVLIQDMNMGKEYKCKVSNKALPAPIEKT 120  
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
DB 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSVMEALHNHYQOQSLSLSPGK 232  
DB 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSVMEALHNHYQOQSLSLSPGK 232  
  
RESULT 9  
AAE26272  
ID AAE26272 standard; protein; 232 AA.  
XX  
AC AAE26272;  
XX  
DT 14-NOV-2002 (first entry)  
XX  
DE Human IgG1 heavy chain.  
XX  
DE Human: amyloidogenic protein; Alzheimer's disease; Huntington's disease;  
XX spongiform encephalopathy; familial amyloid cardiomyopathy; amyloidosis;  
XX Gerstmann-Strausler-Scheinker syndrome; spongiform encephalopathy; GSS;  
XX Creutzfeldt-Jacob disease; insulinoma; diabetes; body myocytis; myeloma;  
XX CJ.  
XX  
XX Homo sapiens.  
XX  
XX WO200242462-A2.  
XX  
XX 30-MAY-2002.  
XX  
XX 27-NOV-2001; 2001WO-US044581.  
XX  
XX 27-NOV-2000; 2000US-0253302P.  
XX  
XX 29-NOV-2000; 2000US-0250198P.  
XX  
XX

PR 20-DEC-2000; 2000US-0257186P.  
XX (PRAE-) PRAECIS PHARM INC.  
XX  
XX  
PI Gelfer ML, Israel DI, Joyal JL, Gosselin M;  
DR MPI; 2002-636427/68.  
XX  
PT Novel therapeutic agent useful for treating an amyloidogenic disorder,  
PT e.g. Alzheimer's disease, comprises an immunoglobulin heavy chain  
PT constant region linked to a peptide capable of binding amyloidogenic  
PT protein.  
XX  
XX Example 8; Page 76; 79pp; English.  
XX  
XX The invention relates to a compound comprising an immunoglobulin (Ig)  
CC heavy chain constant region or its fragment that retains the ability to  
CC bind an Fc receptor linked by a linker group or a direct bond to a  
CC peptide capable of binding an amyloidogenic protein. The invention is  
CC useful for clearing an amyloidogenic protein such as beta-amyloid,  
CC transthyretin (TTR), prion protein (PrP), islet amyloid polypeptide  
CC (IAPP), atrial natriuretic factor (ANF), kappa light chain, lambda light  
CC chain, amyloid A, procalcitonin, cystatin C, beta2-microglobulin, ApoA-I,  
CC gelsolin, calcitonin, fibrinogen, Huntingtin, alpha-synuclein and  
CC lysosome from a subject and for treating an amyloidogenic disorder such  
CC as Alzheimer's disease and spongiform encephalopathy. Disorders treatable  
CC include those caused or characterised by deposits of TTR (eg. familial  
CC amyloid cardiomyopathy), PrP (eg. spongiform encephalopathies, including  
CC scrapie in sheep, bovine spongiform encephalopathy in cows and  
CC Creutzfeldt-Jacob disease (CJ) and Gerstmann-Strausler-Scheinker  
CC syndrome (GSS) in humans), IAPP (eg. insulinoma, adult onset diabetes),  
CC ANF (eg. isolated atrial amyloid), kappa or lambda light chain (eg.  
CC idiopathic amyloidosis, myeloma), amyloid A (eg. amyloidosis), Apo A-I  
CC (eg. hereditary non-neuropathic systemic amyloidosis), Gelsolin (eg.  
CC familial amyloidosis of Finnish type), Fibrinogen (eg. hereditary renal  
CC amyloidosis), Lysosome (eg. hereditary systemic amyloidosis). Other  
CC examples of amyloidogenic disorders include Huntington's disease and  
CC inclusion body myocytis. The present sequence is human IgG1 heavy chain,  
CC used in the exemplification of the invention  
XX  
SQ Sequence 232 AA;  
Query Match 97.2%; Score 1225; DB 5; Length 232;  
Best Local Similarity 97.0%; Pred. No. 1.7e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EFKSCDKHTTCCPCAPABELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 1 EFKSCDKHTTCCPCAPABELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
QY 61 NMYVDGVEVHNKTKRREBOYNSTRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120  
DB 61 NMYVDGVEVHNKTKRREBOYNSTRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120  
QY 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOENNKTTP 180  
DB 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOENNKTTP 180  
QY 122 ISKAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOENNKTTP 180  
DB 122 ISKAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOENNKTTP 180  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVMEALHNHYOQRSLSPGK 232  
DB 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVMEALHNHYOQRSLSPGK 232  
RESULT 10  
ID ADJ65991 standard; protein; 232 AA.  
XX  
AC ADJ65991;  
XX  
XX 06-MAY-2004 (first entry)  
XX  
DE Herpes virus entry mediator-related protein #2.  
XX

KW therapeutic agent; endotoxin induced disease; fusion protein;  
KW Herpes virus entry mediator; HVEM; immunoglobulin Fc domain;  
KW endotoxic shock; human.  
XX  
XX Homo sapiens.  
XX  
XX JP2003128576-A.  
XX  
XX 08-MAY-2003.  
XX  
XX 25-OCT-2001; 2001JP-00328430.  
XX  
XX 25-OCT-2001; 2001JP-00328430.  
XX  
XX (TAIS) TAISHO PHARM CO LTD.  
XX (GENE-) GENE TECHNO SCI KK.  
XX  
XX MPI; 2003-817833/77.  
XX N-PSDB; ADJ65998.  
XX  
XX New therapeutic agent, useful for treating endotoxin induced disease,  
PT comprises fusion protein of Herpes virus entry mediator protein and  
PT immunoglobulin.  
XX  
PS Claim 5; SEQ ID NO 2; 11pp; Japanese.  
XX  
XX The invention comprises a therapeutic agent for treating endotoxin  
CC induced disease, the therapeutic agent contains a fusion protein of the  
CC Herpes virus entry mediator (HVEM) protein and an immunoglobulin Fc  
CC domain. The therapeutic agent of the invention is useful for treating  
CC endotoxin induced disease, such as endotoxic shock. The present amino  
CC acid sequence represents a human protein which is claimed in the  
CC specification.  
XX  
SQ Sequence 232 AA;  
Query Match 97.2%; Score 1225; DB 7; Length 232;  
Best Local Similarity 97.0%; Pred. No. 1.7e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EFKSCDKHTTCCPCAPABELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 1 EFKSCDKHTTCCPCAPABELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
QY 61 NMYVDGVEVHNKTKRREBOYNSTRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120  
DB 61 NMYVDGVEVHNKTKRREBOYNSTRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120  
QY 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOENNKTTP 180  
DB 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOENNKTTP 180  
QY 122 ISKAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOENNKTTP 180  
DB 122 ISKAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGOENNKTTP 180  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVMEALHNHYOQRSLSPGK 232  
DB 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVMEALHNHYOQRSLSPGK 232  
RESULT 11  
ID ADJ57512 standard; protein; 232 AA.  
XX  
XX ADJ57512;  
XX  
XX 06-MAY-2004 (first entry)  
XX  
XX Human IgG1 Fc domain fragment.  
XX  
XX TF, tissue factor; FVIIa, factor VII; anticoagulant; thrombolytic;  
KW cerebroprotective; cytostatic; vasotropic; antithrombotic; antiarthritic;  
KW antiarteriosclerotic; antiinflammatory; antibacterial; immunosuppressive;  
KW hypertensive; cardiant; coagulation Factor VII; human; immunoglobulin G1;  
KW IgG1.  
XX



XX	Hom	sapiens.
XX	WO2004006962-A2.	
XX	22-JAN-2004.	
XX	09-JUL-2003; 2003WO-DK000481.	
XX	12-JUL-2002; 2002DK-00001099.	
XX	(NOVO ) NOVO NORDISK AS.	
XX	Bjorn SE, Nicolsaisen EM, Steensrup TD;	
XX	WPI; 2004-180224/17.	
XX	New compound binding to tissue factor, useful for treating diseases such	
XX	as anglogenesis, ischemia/reperfusion, and rheumatoid arthritis.	
XX	Claim 16; SEQ ID NO 7; 61pp; English.	
XX	The invention relates to a compound (I) binding to tissue factor (TF).	
XX	The compound (I) has the formula A-(Lm)-G, where A is a PVIa	
XX	polypeptide, Lm is an optional linker group, C comprises an	
XX	immunostimulatory effector domain, and (I) binds to TF. (I) inhibits TF-	
XX	mediated activated factor VII (FVIIa) activity. (I) is useful as a	
XX	medicament, and for the manufacture of a medicament for preventing or	
XX	treating disease or disorder associated with pathophysiological TF	
XX	activity. The disease or disorder associated with pathophysiological TF	
XX	activity are deep venous thrombosis, arterial thrombosis, post surgical	
XX	thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal	
XX	coronary angioplasty (PTCA), stroke, cancer, tumor metastasis,	
XX	anglogenesis, ischemia/reperfusion, rheumatoid arthritis, thrombolytic,	
XX	arteriosclerosis and restenosis following angioplasty, acute and chronic	
XX	indications such as inflammation, septic shock, septicemia, hypotension,	
XX	adult respiratory distress syndrome (ARDS), disseminated intravascular	
XX	coagulopathy (DIC), pulmonary embolism, platelet deposition, myocardial	
XX	infarction, or prophylactic treatment of mammals with atherosclerotic	
XX	vessels at risk for thrombosis. The present sequence represents the Fc	
XX	domain fragment of human immunoglobulin G1 (IgG1).	
XX	Sequence 232 AA;	
XX	Query Match 97.2%; Score 1225; DB 8; Length 232;	
XX	Best Local Similarity 97.0%; Pred. 1.7e-88;	
XX	Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0	
QY	1 EPKSCDKTHTCPCPAPBELLGSPSVFLPPPKKDTLMTSRPEVTCVVVDVSHEDPEVKF 60	
DB	1 EPKSCDKTHTCPCPAPBELLGSPSVFLPPPKKDTLMTSRPEVTCVVVDVSHEDPEVKF 60	
QY	61 NMVYGVGVHVNKTCPREQVNSTRVVSVLTVLHONMNGKGEYCKVSNKRLPAPIETK 120	
DB	61 NMVYGVGVHVNKTCPREQVNSTRVVSVLTVLHODMNGEYCKVSNKRLPAPIETK 120	
QY	121 ISKATQPREPOVYTLPSRDELTKNOVSLTCLVKGFGYPSDIAVWESNGQPENNYKTP 180	
DB	121 ISKATQPREPOVYTLPSRDELTKNOVSLTCLVKGFGYPSDIAVWESNGQPENNYKTP 180	
QY	181 PVLDSVGSFPLYSKLTVDKSRNQGVFSCVMHEALHNHYOQRSLSISPGK 232	
DB	181 PVLDSVGSFPLYSKLTVDKSRNQGVFSCVMHEALHNHYOQRSLSISPGK 232	
XX	RESULT 12	
XX	ADRA48992	
XX	ID ADRA48992 standard; peptide; 232 AA.	
XX	AC ADRA48992;	
XX	DT 02-DEC-2004 (first entry)	
XX	Human IgG1 hinge and CH2 region.	

XX anti-anaemic; nephroretropic; human, HuEPO-L-vFc; erythropoietin; ERO;  
KW anaemia; renal disease; cancer chemotherapy; rheumatoid arthritis;  
KW AZT treatment; HIV infection; myelodysplastic syndrome; renal failure.  
XX  
XX Homo sapiens.  
OS  
XX  
XX US2004175824-A1.  
PN  
XX  
XX 09-SEP-2004.  
PD  
XX  
XX 21-JAN-2004; 2004US-00761593.  
PF  
XX  
XX 17-AUG-2001; 2001US-00932812.  
PR  
XX  
XX (SUNL/) SUN L K.  
PA (SUNB/) SUN B N C.  
PA (SUNC/) SUN C R Y.  
XX  
XX Sun LK, Sun BNC, Sun CRY;  
F1  
XX  
XX WPI; 2004-634851/61.  
DR  
XX  
PT New recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin  
PT (HuEPO), a peptide linker, and a human IgG Fc variant, useful for  
PT treating chronic anemia due to renal diseases, cancer chemotherapy, or  
PT rheumatoid arthritis.  
PS  
XX Disclosure; SEQ ID NO 26; 31pp: English.  
PS  
XX A recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin  
CC (HuEPO), a peptide linker, and a human IgG Fc variant, is new.  
CC INDEPENDENT CLAIMS are also included for the following: a chinese hamster  
CC ovary (CHO)-derived cell line producing the HuEPO-L-vFc fusion protein in  
CC its growth medium in excess of 10 microg per million cells in a 24 hour  
CC period; and a method for making a recombinant fusion protein comprising  
CC HuEPO, a flexible peptide linker, and a human IgG Fc variant. Preferred  
CC protein: The peptide linker containing 20 or fewer amino acids is present  
CC between HuEPO and the human IgG Fc variant, and comprises two or more  
CC amino acids selected from glycine, serine, alanine, and threonine. The  
CC human IgG Fc variant comprises a hinge, CH2, and CH3 domains of human  
CC IgG2 with Pro331Ser mutation comprising 436 amino acids (SEQ ID NO. 18).  
CC It also comprises a hinge, CH2, and CH3 domains of human IgG4 with  
CC Ser228Pro and Leu235Ala mutations comprising 437 amino acids (SEQ ID NO.  
CC 20). It further comprises a hinge, CH2, and CH3 domains of human IgG1  
CC with Leu234Val, Leu235Ala, and Pro331Ser mutations comprising 435 amino  
CC acids (SEQ ID NO. 22). The HuEPO-L-vFc fusion protein exhibits in vitro  
CC biological activity similar to or higher than that of rHuEPO on a molar  
CC basis. Preferred CHO-Derived Cell Line: The CHO-derived cell line  
CC producing the HuEPO-L-vFc fusion protein in its growth medium in excess  
CC of 30 microg per million cells in a 24 hour period. The human IgG Fc  
CC variant comprises a hinge, CH2, CH3 domains of human IgG selected from  
CC IgG1 as SEQ ID NO. 22, IgG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20.  
CC The IgG Fc contains amino acid mutations to attenuate effector functions,  
CC a flexible peptide linker containing 20 or fewer amino acids is present  
CC between HuEPO and human IgG Fc variant, and the HuEPO-L-vFc fusion  
CC protein exhibits in vitro biological activity similar to or higher than  
CC that of rHuEPO on a molar basis. Preferred Method: Making a recombinant  
CC fusion protein comprising HuEPO, a flexible peptide linker, and a human  
CC IgG Fc variant comprises: generating a CHO-derived cell line; growing the  
CC cell line where the recombinant protein is expressed in its growth medium  
CC in excess of 10 microg per million cells in a 24 hour period; and  
CC purifying the expressed protein from (b), where the recombinant fusion  
CC protein exhibits in vitro biological activity similar to or higher than  
CC that of rHuEPO on a molar basis. Antianemic; Nephroretropic. No biological  
CC data given. None given. Administration can be through subcutaneous or  
CC intravenous route. No dosage given. The recombinant HuEPO-L-vFc fusion  
CC protein is useful for treating patients with chronic anemia due to renal  
CC diseases, cancer chemotherapy, rheumatoid arthritis, AZT treatment for  
CC HIV infection, or myelodysplastic syndrome. It is also useful in the  
CC treatment of renal failure. A fusion protein was assembled from several  
CC DNA segments to obtain the gene encoding the leader peptide and mature  
CC protein of human erythropoietin (EPO), cDNA library of human fetal liver

or kidney was used as the template in polymerase chain reaction (PCR). For the convenience of cloning, SEQ ID NO. 1 which incorporates a restriction enzyme cleavage site is used as the 5' oligonucleotide primer. The 3' primer (SEQ ID NO. 2) eliminates the EPO termination codon and incorporates a BamHI site. The resulting DNA fragments of approximately 600 bp were inserted into a holding vector such as pUC19 at CC the HindIII and BamHI sites to give the pEPO plasmid. The sequence of the human EPO gene was confirmed by DNA sequencing.

Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 8; Length 232;

Best Local Similarity 97.0%; Pred. No. 1.7e-88;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 EPKSCDKHTHTCPCPAPBELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 1 EPKSCDKHTHTCPCPAPBELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 61 NMVYDGVENVNKTYPREQVNSTYRVSVLTTLHQMNGKKEYCKVSNKALPAPIETK 120  
 61 NMVYDGVENVNKTYPREQVNSTYRVSVLTTLHQMNGKKEYCKVSNKALPAPIETK 120  
 121 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTP 180  
 121 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTP 180  
 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSYMHEALHNHYOQRSLSIPGK 232  
 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSYMHEALHNHYOQRSLSIPGK 232

#### RESULT 13

AB09463 standard; protein; 233 AA.

AB09463;

01-JUL-2002 (first entry)

Human IgG Fc fragment amino acid sequence.

Protein A; immunoglobulin G; IgG; antibody; human.

Homo sapiens.

Key Location/Qualifiers

Misc-difference 168 /note= "encoded by GAC"

Misc-difference 169 /note= "encoded by ACC"

WO200204602-A1.

17-JAN-2002.

04-JUL-2001; 2001WO-JP005788.

07-JUL-2000; 2000JP-00206689.

(GENC-) GENCOM CORP.

Tanaka A, Ueda M, Teranishi Y;

WPI; 2002-148174/19.

N-PSDB; ABL52834.

Transformant yeast for stable supply of highly active catalytic antibody, comprises the capability of expressing and presenting protein A or its fragment, particularly with the 22 domain, on the cell surface.  
 Example 3; Fig 4; 25pp; Japanese.

The invention relates to a transformant yeast that can present protein A or its fragment on its cell surface. The yeast can be used for detecting or isolating the Fc part of immunoglobulin (Ig)G. The yeast is useful for a stable supply of highly active catalytic antibody e.g. by screening novel functional molecules and in isolating Fc-carrying secretory proteins. The yeast of the invention is capable of adhering specifically to a combinatorial antibody library with an Fc-carrying antibody component. The current sequence represents the human IgG Fc fragment amino acid sequence

Sequence 233 AA;

Query Match 97.2%; Score 1225; DB 5; Length 233;

Best Local Similarity 97.0%; Pred. No. 1.7e-88;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 EPKSCDKHTHTCPCPAPBELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 2 EPKSCDKHTHTCPCPAPBELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 61  
 61 NMVYDGVENVNKTYPREQVNSTYRVSVLTTLHQMNGKKEYCKVSNKALPAPIETK 120  
 62 NMVYDGVENVNKTYPREQVNSTYRVSVLTTLHQMNGKKEYCKVSNKALPAPIETK 121  
 121 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTP 180  
 122 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTP 181  
 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSYMHEALHNHYOQRSLSIPGK 232  
 183 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSYMHEALHNHYOQRSLSIPGK 233

#### RESULT 14

ABJ38647 standard; protein; 235 AA.

ABJ38647;

26-JUN-2003 (first entry)

PCXFc protein SEQ ID No 6.

Cytostatic; osteopathic; cerebroprotective; dermatological; enzyme; antigen binding; receptor protein tyrosine kinase; skeletal dysplasia;

constitutive activation; craniosynostosis; cell proliferative disorder; achondroplasia; thanatophoric dysplasia; acanthosis nigricans dysplasia;

hypochondroplasia; severe achondroplasia; transitional cell carcinoma; Muenke coronal craniosynostosis; Crouzin syndrome; acanthosis nigricans;

tumour progression; osteosarcoma; chondrosarcoma; multiple myeloma; mammary carcinoma; fibroblast growth factor receptor 3; FGFR3 protein.

Homo sapiens.

WO2002102854-A2.

27-DEC-2002.

20-JUN-2002; 2002WO-IB003523.

20-JUN-2001; 2001US-0299187P.

(MORP-) MORPHOSYS AG.

(PROC-) PROCHON BIOTECH LTD.

Thomassen-Wolf E, Borges E, Yayon A, Rom E;

WPI; 2003-167489/16.

N-PSDB; ABL40262.

New molecules having the antigen-binding portion of antibodies that block activation of receptor protein tyrosine kinase, useful for treating or inhibiting skeletal dysplasias, craniosynostosis or cell proliferative

PT disorders.

PS Example 2; Page 38; 103pp; English.

The invention relates to a novel molecule comprising the antigen binding portion of an isolated antibody, which has an increased affinity for a receptor protein tyrosine kinase and which blocks constitutive activation of the receptor protein tyrosine kinase. The methods and compositions of the invention are useful for treating or inhibiting a skeletal dysplasia, craniosynostosis or a cell proliferative disorder. The skeletal dysplasia is achondroplasia, thanatophoric dysplasia, hypochondroplasia, severe achondroplasia with developmental delay or acanthosis nigricans dysplasia. The craniosynostosis disorder is Muenke coronal craniosynostosis or Crouzon syndrome with acanthosis nigricans. The cell proliferative disorder is tumour progression that is progression of transitional cell carcinoma, osteosarcoma, chondrosarcoma, multiple myeloma or mammary carcinoma. This sequence represents a protein derived from a pCpXc plasmid DNA vector relating to the protein tyrosine kinase inhibitor of the invention.

**SQ** Sequence 235 AA;

Query Match	97.2%	Score 1225	DB 6	Length 235
Best Local Similarity	97.0%	Pred. No. 1.7e-88		
Matches 225	Conservative 3	Mismatches 4	Indels 0	Gaps 0

Qy	1	EPKSCDKHTCCPCAPBELLGSPVFLPPPKYKOTLMSTRPEYTCVVDVSHDEPVK	60
Db	4	EPKSCDKHTCCPCAPBELLGSPVFLPPPKYKOTLMSTRPEYTCVVDVSHDEPVK	63
Qy	61	NWYVDGEVHNHYKTRKEEQYNSTRVWSVLTVLHQNMNNGKEYCKKVSNNKLPAPIEKT	120
Db	64	NWYVDGEVHNHYKTRKEEQYNSTRVWSVLTVLHQDMLNGKEYCKKVSNNKLPAPIEKT	123
Qy	121	ISKAKVQPREPOVYITLPPSRDELTKNQVSLTCLVKGYPSDIAVEWESNGQPENNYKTTTP	180
Db	124	ISKAKVQPREPOVYITLPPSRDELTKNQVSLTCLVKGYPSDIAVEWESNGQPENNYKTTTP	183
Qy	181	PVLDSDGSGFELYSKLTVDKSRWQGNVSSCSYMEHALLNNHYQQSLSLSPCK	232
Db	184	PVLDSDGSGFELYSKLTVDKSRWQGNVSSCSYMEHALLNNHYQQSLSLSPCK	235

## RESULT 15

ID ADA89055 standard; protein; 235 AA.

AC ADA89055;

DT 20-NOV-2003 (first entry)

Plasmid pCXFc amino acid sequence SEQ ID NO:6

KM antigen binding; antibody; specific binding affinity;  
KM receptor protein tyrosine kinase; RPK;  
KM receptor protein tyrosine kinase inhibitor;  
KM fibroblast growth factor receptor; FGFR; osteopathic; cytostatic;  
KM ophthalmological; bone disorder; cartilage disorder; skeletal disorder  
KM skeletal dysplasia; chondroosteosarcoma; chondroectodermal dysplasia;  
KM hypochondroplasia; cranioosteoarthritis; disorder;  
KM malignant cell proliferative disease; cancer; tumour; vision disorder;  
KM non-neoplastic proliferative pathologic condition;

OS Synthetic.

XX

XX

XX

XX XX

PA (PROC-) PROCHON BIOTECH LTD

PI Yayon A, Rom E;

DR WPI; 2003-175236/17.

XX

PT New antibodies which have specific binding affinity for a receptor  
PT protein tyrosine kinase (RPTK) and block constitutive activation of  
PT useful for treating bone and cartilage disorders, or malignant cell  
PT proliferative diseases.

PS Example 2; Page 43; 122pp; English.

The present invention describes a molecule (1) comprising the antigen binding portion of an isolated antibody which has specific binding affinity for a receptor protein tyrosine kinase (RPTK), particularly for a fibroblast growth factor receptor (FGFR), and which blocks constitutive activation of an RPTK. Also described: (1) pharmaceutical compositions comprising (1) as an active ingredient and a pharmaceutical carrier, excipient or auxiliary agent; (2) a kit comprising (1), at least one reagent for detecting the presence of (1) when bound to the RPTK, and instructions for use; (3) a method for treatment of bone and cartilage related disorders by administering a composition of (1) to the subject; (4) a method for treating or inhibiting a cell proliferative disease or disorder by administering the composition of (1); (5) a method for screening a molecule comprising the antigen-binding portion of an antibody which blocks ligand-dependent activation of RPTK; (6) an isolated nucleic acid molecule encoding a VL-CDR3 DNA region and a VH-CDR3 DNA region; (7) an isolated nucleic acid molecule encoding VL region and a VH region; (8) vectors comprising a nucleic acid molecule of (6) or (7); and (9) host cells transformed with the vector. (1) have osteopontic, cyostatic and ophthalmological activities, and can be used as a RPTK inhibitor. Compositions comprising (1) are useful for treating bone and cartilage disorders, including skeletal disorders such as skeletal dysplasia (achondroplasia, thanatophoric dysplasia, hypochondroplasia, severe achondroplasia with developmental delay and acanthosis nigricans dysplasia) or a craniosynostosis disorder (e.g. Muenke coronal craniosynostosis or Crouzon syndrome with acanthosis nigricans). The composition may also be used for treating or inhibiting malignant cell proliferative disease or disorder associated with abnormal RPTK activity, including a haematopoietic malignancy (e.g. multiple myeloma), solid tumours (e.g. mammary, colon, cervical, bladder, colorectal, chondrosarcoma or osteosarcoma), tumour formation, primary tumour, tumour progression (particularly progression of transitional cell carcinoma or mammary carcinoma), or tumour metastasis, where the cell proliferative disorder may be associated with the action of a constitutively activated RPTK, or with ligand-dependent activation of RPTK. The compositions may further be used for treating hyperproliferative diseases and disorders associated with ligand-dependent FGFR signaling, such as vision disorders (e.g. neovascular glaucoma, macular degeneration and proliferative retinopathy including diabetic retinopathy), and non-neoplastic angiogenic pathologic conditions (e.g. haemangiomas, angiodiomas and psoriasis). The present sequence is given in the exemplification of the present invention.

Sequence 235 AA;

Query Match	97.2%	Score 1235	DB 6	Length 235
Best Local Similarity	97.0%	Pred. 1.7e-88		
Matches 225		Conservative 3	Mismatches 4	Indels 0
				Gaps 0

Qy	1	EPKSKCDKHTHCPCAPAPELGLGSPVFLPPKPKDLMIRTEVTCVYVDVSHEDPEVK	60
Db	4	EPKSCDKHTHCPCAPAPELGLGSPVFLPPKPKDLMIRTEVTCVYVDVSHEDPEVK	63
Qy	61	NWYVDGVEVHNKTKPREQYNSTRVSVLTVLQHNMNNGKYEKKCVSNKALPAPIEKT	120
Db	64	NWYVDGVEVHNKTKPREQYNSTRVSVLTVLQHNMNNGKYEKKCVSNKALPAPIEKT	123
Qy	121	ISKATVQPREPOVYTLPSGRDELTKQVSLTCLVKGFTYSDIATVWESNGQPENNYKTTTP	180

Db 124 ISKAGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTT 183  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQSYMHEALNNHYOQRSLSLSPGK 232  
Db 184 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQSYMHEALNNHYOQRSLSLSPGK 235

Search completed: June 7, 2005, 08:56:39  
Job time : 119.803 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: June 7, 2005, 09:01:44 ; Search time 101.775 Seconds  
(without alignments)  
821.093 Million cell updates/sec

Title: US-10-000-439-3

Perfect score: 1260  
Sequence: 1 EPKSCDKHTHTCPCPAPPELL.....MHEALHNYQQRSLSLSPGK 232

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1599520 seqs, 360203123 residues

Total number of hits satisfying chosen parameters: 1599520

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_Aa:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*

12: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*

13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*

16: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*

17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

19: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*

20: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

21: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1260	100.0	232	10 US-09-847-208-3	Sequence 3, Appl1
2	1260	100.0	232	14 US-10-000-439-3	Sequence 3, Appl1
3	1260	100.0	330	10 US-09-847-208-2	Sequence 2, Appl1
4	1260	100.0	330	14 US-10-000-439-2	Sequence 2, Appl1
5	1260	100.0	569	10 US-09-847-208-7	Sequence 7, Appl1
6	1260	100.0	569	14 US-10-000-439-7	Sequence 7, Appl1
7	1225	97.2	232	9 US-09-996-357-10	Sequence 10, Appl1
8	1225	97.2	232	10 US-09-389-782-1	Sequence 1, Appl1
9	1225	97.2	232	16 US-10-617-619-7	Sequence 7, Appl1
10	1225	97.2	232	16 US-10-761-593A-26	Sequence 26, Appl1
11	1225	97.2	232	16 US-10-831-622-97	Sequence 97, Appl1
12	1225	97.2	232	16 US-10-800-497-26	Sequence 26, Appl1

13	1225	97.2	232	16 US-10-800-449-26	Sequence 26, Appl1
14	1225	97.2	235	14 US-10-207-655-208	Sequence 208, App
15	1225	97.2	247	9 US-09-996-357-13	Sequence 13, Appl1
16	1225	97.2	251	14 US-10-008-063-18	Sequence 18, Appl1
17	1225	97.2	251	14 US-10-152-363A-6	Sequence 6, Appl1
18	1225	97.2	267	9 US-09-966-357-12	Sequence 12, Appl1
19	1225	97.2	288	10 US-09-822-851B-14	Sequence 14, Appl1
20	1225	97.2	288	14 US-10-119-637A-14	Sequence 14, Appl1
21	1225	97.2	329	15 US-10-370-749-48	Sequence 48, Appl1
22	1225	97.2	329	16 US-10-798-380-37	Sequence 37, Appl1
23	1225	97.2	330	10 US-09-995-898A-15	Sequence 15, Appl1
24	1225	97.2	330	10 US-09-892-949-38	Sequence 38, Appl1
25	1225	97.2	330	13 US-10-047-542-20	Sequence 20, Appl1
26	1225	97.2	330	14 US-10-269-805-68	Sequence 68, Appl1
27	1225	97.2	330	14 US-10-310-719-8	Sequence 8, Appl1
28	1225	97.2	330	14 US-10-112-582-1	Sequence 1, Appl1
29	1225	97.2	330	14 US-10-330-231A-81	Sequence 81, Appl1
30	1225	97.2	330	15 US-10-383-902A-6	Sequence 6, Appl1
31	1225	97.2	330	15 US-10-408-901-2	Sequence 2, Appl1
32	1225	97.2	330	15 US-10-420-034A-15	Sequence 15, Appl1
33	1225	97.2	330	15 US-10-257-907-5	Sequence 5, Appl1
34	1225	97.2	330	15 US-10-656-769-2	Sequence 2, Appl1
35	1225	97.2	330	16 US-10-679-620-58	Sequence 58, Appl1
36	1225	97.2	330	16 US-10-772-531-38	Sequence 38, Appl1
37	1225	97.2	330	16 US-10-479-326-1	Sequence 1, Appl1
38	1225	97.2	330	16 US-10-815-449-8	Sequence 8, Appl1
39	1225	97.2	331	9 US-09-761-413-2	Sequence 2, Appl1
40	1225	97.2	331	14 US-10-341-836-2	Sequence 2, Appl1
41	1225	97.2	331	16 US-10-473-127-1863	Sequence 1663, Ap
42	1225	97.2	332	10 US-09-990-586-98	Sequence 98, Appl1
43	1225	97.2	332	14 US-10-310-113-167	Sequence 167, App
44	1225	97.2	332	14 US-10-230-680-98	Sequence 98, Appl1
45	1225	97.2	333	15 US-10-272-899A-8	Sequence 8, Appl1

#### ALIGNMENTS

RESULT 1

US-09-847-208-3

Sequence 3, Application US/09847208

Publication No. US20030082190A1

GENERAL INFORMATION:

APPLICANT: Saxon, Andrew

APPLICANT: Zhu, Daocheng

TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF

TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES

FILE REFERENCE: UC67.002A

CURRENT APPLICATION NUMBER: US/09/847,208

CURRENT FILING DATE: 2001-05-01

NUMBER OF SEQ ID NOS: 177

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 232

TYPE: PRT

ORGANISM: Homo sapiens

US-09-847-208-3

Query Match	100.0%	Score 1260;	DB 10;	Length 232;
Best Local Similarity	100.0%;	Pred. No. 9.8e-93;		
Matches	232;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	

QY	1	EPKSCDKHTHTCPCPAPPELLGSPSFLPPPKKDTLMTSRTPRYTCVVVDVSHEDPEVKF	60
DB	1	EPKSCDKHTHTCPCPAPPELLGSPSFLPPPKKDTLMTSRTPRYTCVVVDVSHEDPEVKF	60
QY	61	MYVGVGVHVNKTPREBOVNSTYRVSVLTFLHQMNGGKRYCKYSNKLPAPIEKT	120
DB	61	MYVGVGVHVNKTPREBOVNSTYRVSVLTFLHQMNGGKRYCKYSNKLPAPIEKT	120
QY	121	ISKAVQPREPOVYTLPPSRDELITNOVSLTGVKGFYPSDIAEWESNGOENNYKTPP	180

Db 121 ISKAVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTP 180  
Qy 181 PVLDSVGSFPLYSKLTVDKSRWQOGNVFSCSVMEHALNHHYQORSLISLSPGK 232  
Db 181 PVLDSVGSFPLYSKLTVDKSRWQOGNVFSCSVMEHALNHHYQORSLISLSPGK 232

RESULT 2  
US-10-000-439-3  
; Sequence 3, Application US/10000439  
; Publication No. US20030064063A1  
; GENERAL INFORMATION:  
; APPLICANT: Saxon, Andrew  
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR  
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES  
; FILE REFERENCE: UC067.004A  
; CURRENT APPLICATION NUMBER: US/10/000.439  
; CURRENT FILING DATE: 2001-10-24  
; PRIOR APPLICATION NUMBER: US 09/847,208  
; PRIOR FILING DATE: 2001-05-01  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-000-439-3

Query Match 100.0%; Score 1260; DB 14; Length 232;  
Best Local Similarity 100.0%; Pred. No. 9.8e-93;  
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPKSCDKHTHTCPGPCAPPELLGSPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
Db 1 EPKSCDKHTHTCPGPCAPPELLGSPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
Qy 61 NMVYDGEVHNKTKPREEOYNSTRVAVSVLTVLHONMNGKEYCKVSNKALPAPIEKT 120  
Db 61 NMVYDGEVHNKTKPREEOYNSTRVAVSVLTVLHONMNGKEYCKVSNKALPAPIEKT 120  
Qy 121 ISKAVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTP 180  
Db 121 ISKAVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTP 180  
Qy 181 PVLDSVGSFPLYSKLTVDKSRWQOGNVFSCSVMEHALNHHYQORSLISLSPGK 232  
Db 181 PVLDSVGSFPLYSKLTVDKSRWQOGNVFSCSVMEHALNHHYQORSLISLSPGK 232

RESULT 3  
US-09-847-208-2  
; Sequence 2, Application US/09847208  
; Publication No. US20030082190A1  
; GENERAL INFORMATION:  
; APPLICANT: Saxon, Andrew  
; APPLICANT: Zhang, Ke  
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF  
; TITLE OF INVENTION: 19E-MEDIATED ALLERGIC DISEASES  
; FILE REFERENCE: UC67.002A  
; CURRENT APPLICATION NUMBER: US/09/847,208  
; CURRENT FILING DATE: 2001-05-01  
; NUMBER OF SEQ ID NOS: 177  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 330  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-847-208-2

Query Match 100.0%; Score 1260; DB 10; Length 330;  
Best Local Similarity 100.0%; Pred. No. 1.5e-92;  
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPKSCDKHTHTCPGPCAPPELLGSPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
Db 99 EPKSCDKHTHTCPGPCAPPELLGSPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 158  
Qy 61 NMVYDGEVHNKTKPREEOYNSTRVAVSVLTVLHONMNGKEYCKVSNKALPAPIEKT 120  
Db 159 NMVYDGEVHNKTKPREEOYNSTRVAVSVLTVLHONMNGKEYCKVSNKALPAPIEKT 218  
Qy 121 ISKAVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTP 180  
Db 219 ISKAVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTP 278  
Qy 181 PVLDSVGSFPLYSKLTVDKSRWQOGNVFSCSVMEHALNHHYQORSLISLSPGK 232  
Db 279 PVLDSVGSFPLYSKLTVDKSRWQOGNVFSCSVMEHALNHHYQORSLISLSPGK 330

RESULT 4  
US-10-000-439-2  
; Sequence 2, Application US/10000439  
; Publication No. US20030064063A1  
; GENERAL INFORMATION:  
; APPLICANT: Saxon, Andrew  
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR  
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES  
; FILE REFERENCE: UC067.004A  
; CURRENT APPLICATION NUMBER: US/10/000.439  
; CURRENT FILING DATE: 2001-10-24  
; PRIOR APPLICATION NUMBER: US 09/847,208  
; PRIOR FILING DATE: 2001-05-01  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 330  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-000-439-2

Query Match 100.0%; Score 1260; DB 14; Length 330;  
Best Local Similarity 100.0%; Pred. No. 1.5e-92;  
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPKSCDKHTHTCPGPCAPPELLGSPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
Db 99 EPKSCDKHTHTCPGPCAPPELLGSPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 158  
Qy 61 NMVYDGEVHNKTKPREEOYNSTRVAVSVLTVLHONMNGKEYCKVSNKALPAPIEKT 120  
Db 159 NMVYDGEVHNKTKPREEOYNSTRVAVSVLTVLHONMNGKEYCKVSNKALPAPIEKT 218  
Qy 121 ISKAVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTP 180  
Db 219 ISKAVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTP 278  
Qy 181 PVLDSVGSFPLYSKLTVDKSRWQOGNVFSCSVMEHALNHHYQORSLISLSPGK 232  
Db 279 PVLDSVGSFPLYSKLTVDKSRWQOGNVFSCSVMEHALNHHYQORSLISLSPGK 330

RESULT 5  
US-09-847-208-7  
; Sequence 7, Application US/09847208  
; Publication No. US20030082190A1  
; GENERAL INFORMATION:  
; APPLICANT: Saxon, Andrew  
; APPLICANT: Zhang, Ke  
; APPLICANT: Zhu, Daocheng  
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF  
; TITLE OF INVENTION: 19E-MEDIATED ALLERGIC DISEASES  
; FILE REFERENCE: UC67.002A  
; CURRENT APPLICATION NUMBER: US/09/847,208  
; CURRENT FILING DATE: 2001-05-01

; NUMBER OF SEQ ID NOS: 177  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 569  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Fusion between hinge-CH2-CH3 (IgG1) to CH2-CH3-CH4  
US-09-847-208-7

Query Match 100.0%; Score 1260; DB 10; Length 569;  
Best Local Similarity 100.0%; Pred. No. 2.8e-92;  
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
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DB 61 NMYVDGVEVHNVKTPREBQYNSTYRVVSVLTVLHQNMNNGKEYCKCKVSNKALPAPIEKT 120  
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTP 180  
DB 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTP 180  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVMHREALNHYOQRLSLSPGK 232  
DB 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVMHREALNHYOQRLSLSPGK 232

## RESULT 6

US-10-000-439-7  
; Sequence 7, Application US/10000439  
; Publication No. US20030064063A1  
; GENERAL INFORMATION:  
; APPLICANT: Saxon, Andrew  
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR  
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES  
; FILE REFERENCE: UC067.004A  
; CURRENT APPLICATION NUMBER: US/10/000,439  
; CURRENT FILING DATE: 2001-10-24  
; PRIOR APPLICATION NUMBER: US 09/847,208  
; PRIOR FILING DATE: 2001-05-01  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 569  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Fusion polypeptide comprising a hinge-CH2-CH3  
; OTHER INFORMATION: (IgG1) sequence and a CH2-CH3-CH4 (IgE) sequence  
US-10-000-439-7

Query Match 100.0%; Score 1260; DB 14; Length 569;  
Best Local Similarity 100.0%; Pred. No. 2.8e-92;  
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
DB 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
QY 61 NMYVDGVEVHNVKTPREBQYNSTYRVVSVLTVLHQNMNNGKEYCKCKVSNKALPAPIEKT 120  
DB 61 NMYVDGVEVHNVKTPREBQYNSTYRVVSVLTVLHQNMNNGKEYCKCKVSNKALPAPIEKT 120  
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTP 180  
DB 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTP 180  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVMHREALNHYOQRLSLSPGK 232

DB 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVMHREALNHYOQRLSLSPGK 232

## RESULT 7

US-09-996-357-10  
; Sequence 10, Application US/09996357  
; Patent No. US20020133001A1  
; GENERAL INFORMATION:  
; APPLICANT: Gelfert, Malcolm L  
; APPLICANT: Isreal, David I  
; APPLICANT: Joyal, John L  
; APPLICANT: Gosselin, Michael  
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR  
; TITLE OF INVENTION: TREATING AN AMYLOIDOTIC DISEASE  
; FILE REFERENCE: PPI-105  
; CURRENT APPLICATION NUMBER: US/09/996,357  
; CURRENT FILING DATE: 2001-11-27  
; PRIOR APPLICATION NUMBER: 60/253,302  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/250,198  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: 60/257,186  
; PRIOR FILING DATE: 2000-12-20  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-357-10

Query Match 97.2%; Score 1225; DB 9; Length 232;  
Best Local Similarity 97.0%; Pred. No. 6.1e-90;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
DB 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
QY 61 NMYVDGVEVHNVKTPREBQYNSTYRVVSVLTVLHQNMNNGKEYCKCKVSNKALPAPIEKT 120  
DB 61 NMYVDGVEVHNVKTPREBQYNSTYRVVSVLTVLHQNMNNGKEYCKCKVSNKALPAPIEKT 120  
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTP 180  
DB 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTP 180  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVMHREALNHYOQRLSLSPGK 232  
DB 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVMHREALNHYOQRLSLSPGK 232

## RESULT 8

US-09-389-782-1  
; Sequence 1, Application US/09389782  
; Publication No. US20030144187A1  
; GENERAL INFORMATION:  
; APPLICANT: Wooden, Scott K.  
; APPLICANT: Mann, Michael B.  
; APPLICANT: Dunstan, Colin R.  
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods  
; FILE REFERENCE: A-604  
; CURRENT APPLICATION NUMBER: US/09/389,782  
; CURRENT FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Human  
US-09-389-782-1

Query Match 97.2%; Score 1225; DB 10; Length 232;  
Best Local Similarity 97.0%; Pred. No. 6, 1e-90;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPBLGSPVFLFPKPKDTLMTISRTPEVTCVVVDVSHEDPEVKF 60  
DB 1 EPKSCDKHTHTCPCPAPBLGSPVFLFPKPKDTLMTISRTPEVTCVVVDVSHEDPEVKF 60  
QY 61 NMYVDGVEVHNAKTKPREEOYNSTRYVSVLTVLHQNMMNGEKYCKVSNKALPAPIEKT 120  
DB 61 NMYVDGVEVHNAKTKPREEOYNSTRYVSVLTVLHQNMMNGEKYCKVSNKALPAPIEKT 120  
QY 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVMESNGOPENNYKTTTP 180  
DB 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVMESNGOPENNYKTTTP 180  
QY 181 PVLDSGSPFLYSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSISPGK 232  
DB 181 PVLDSGSPFLYSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSISPGK 232

RESULT 9  
US-10-617-619-7  
; Sequence 7, Application US/10617619  
; Publication No. US20040110929A1  
; GENERAL INFORMATION:  
; APPLICANT: Bjorn, Soren E  
; APPLICANT: Nicolaesen, Else M  
; APPLICANT: Jorgensen, Anker S  
; TITLE OF INVENTION: TF Binding Compound  
; FILE REFERENCE: 6455,200-US  
; CURRENT APPLICATION NUMBER: US/10/617,619  
; CURRENT FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01099  
; PRIOR FILING DATE: 2002-07-12  
; PRIOR APPLICATION NUMBER: US 60/404,568  
; PRIOR FILING DATE: 2002-08-19  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Human  
US-10-617-619-7

Query Match 97.2%; Score 1225; DB 16; Length 232;  
Best Local Similarity 97.0%; Pred. No. 6, 1e-90;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPBLGSPVFLFPKPKDTLMTISRTPEVTCVVVDVSHEDPEVKF 60  
DB 1 EPKSCDKHTHTCPCPAPBLGSPVFLFPKPKDTLMTISRTPEVTCVVVDVSHEDPEVKF 60  
QY 61 NMYVDGVEVHNAKTKPREEOYNSTRYVSVLTVLHQNMMNGEKYCKVSNKALPAPIEKT 120  
DB 61 NMYVDGVEVHNAKTKPREEOYNSTRYVSVLTVLHQNMMNGEKYCKVSNKALPAPIEKT 120  
QY 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVMESNGOPENNYKTTTP 180  
DB 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVMESNGOPENNYKTTTP 180  
QY 181 PVLDSGSPFLYSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSISPGK 232  
DB 181 PVLDSGSPFLYSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSISPGK 232

RESULT 10  
US-10-761-593A-26  
; Sequence 26, Application US/10761593A  
; Publication No. US20040175824A1  
; GENERAL INFORMATION:  
; APPLICANT: Sun, Lee-Hwei K  
; APPLICANT: Sun, Bill N

; APPLICANT: Sun, Cecily R  
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological  
; TITLE OF INVENTION: activities  
; FILE REFERENCE: 02SUN2001-A  
; CURRENT APPLICATION NUMBER: US/10/761,593A  
; CURRENT FILING DATE: 2004-01-21  
; PRIOR APPLICATION NUMBER: 09/932812  
; PRIOR FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 26  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-761-593A-26

Query Match 97.2%; Score 1225; DB 16; Length 232;  
Best Local Similarity 97.0%; Pred. No. 6, 1e-90;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPBLGSPVFLFPKPKDTLMTISRTPEVTCVVVDVSHEDPEVKF 60  
DB 1 EPKSCDKHTHTCPCPAPBLGSPVFLFPKPKDTLMTISRTPEVTCVVVDVSHEDPEVKF 60  
QY 61 NMYVDGVEVHNAKTKPREEOYNSTRYVSVLTVLHQNMMNGEKYCKVSNKALPAPIEKT 120  
DB 61 NMYVDGVEVHNAKTKPREEOYNSTRYVSVLTVLHQNMMNGEKYCKVSNKALPAPIEKT 120  
QY 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVMESNGOPENNYKTTTP 180  
DB 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVMESNGOPENNYKTTTP 180  
QY 181 PVLDSGSPFLYSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSISPGK 232  
DB 181 PVLDSGSPFLYSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSISPGK 232

RESULT 11  
US-10-831-622-97  
; Sequence 97, Application US/10831622  
; Publication No. US20040248257A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaye, Jonathan  
; APPLICANT: Wilkinson, Beverley  
; TITLE OF INVENTION: SPEX COMPOSITIONS AND METHODS OF USE  
; FILE REFERENCE: TSRI 810.1  
; CURRENT APPLICATION NUMBER: US/10/831,622  
; CURRENT FILING DATE: 2004-04-23  
; PRIOR APPLICATION NUMBER: US 60/467,206  
; PRIOR FILING DATE: 2003-04-30  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 97  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-831-622-97

Query Match 97.2%; Score 1225; DB 16; Length 232;  
Best Local Similarity 97.0%; Pred. No. 6, 1e-90;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPBLGSPVFLFPKPKDTLMTISRTPEVTCVVVDVSHEDPEVKF 60  
DB 1 EPKSCDKHTHTCPCPAPBLGSPVFLFPKPKDTLMTISRTPEVTCVVVDVSHEDPEVKF 60  
QY 61 NMYVDGVEVHNAKTKPREEOYNSTRYVSVLTVLHQNMMNGEKYCKVSNKALPAPIEKT 120  
DB 61 NMYVDGVEVHNAKTKPREEOYNSTRYVSVLTVLHQNMMNGEKYCKVSNKALPAPIEKT 120  
QY 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVMESNGOPENNYKTTTP 180  
DB 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIIVMESNGOPENNYKTTTP 180



**Query** 181 PVLDSVGSFFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232  
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**Db** 181 PVLDSGGSFFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYQKSLSLSPGK 232  
 |||||

**RESULT 12**  
 US-10-800-497-26  
 : Sequence 26, Application US/10800497  
 : Publication No. US20040259209A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Sun, Lee-Hwei K  
 : APPLICANT: Sun, Bill  
 : APPLICANT: Sun, Cecily R  
 : TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor with  
 : TITLE OF INVENTION: stimulating factor with  
 : TITLE OF INVENTION: increased biological activities  
 : FILE REFERENCE: 03SUN2001  
 : CURRENT APPLICATION NUMBER: US/10/800,497  
 : CURRENT FILING DATE: 2004-03-15  
 : PRIOR APPLICATION NUMBER: US/09/968,362  
 : PRIOR FILING DATE: 2001-10-01  
 : NUMBER OF SEQ ID NOS: 28  
 : SOFTWARE: PatentIn version 3.1  
 : SEQ ID NO 26  
 : LENGTH: 232  
 : TYPE: PRT  
 : ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains  
 US-10-800-497-26

**Query Match** 97.2% Score 1225; DB 16; Length 232;  
 Best Local Similarity 97.0%; Pred. No. 6,1e-90;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

**QY** 1 EPKSCDKHTHTPCPCAPAPLGLGSPVFLPPPKKQDTLMTSRTPETVCVVYDVSHEDPEVKF 60  
 1 EPKSCDKHTHTPCPCAPAPLGLGSPVFLPPPKKQDTLMTSRTPETVCVVYDVSHEDPEVKF 60  
**DB** 1 EPKSCDKHTHTPCPCAPAPLGLGSPVFLPPPKKQDTLMTSRTPETVCVVYDVSHEDPEVKF 60  
 1 EPKSCDKHTHTPCPCAPAPLGLGSPVFLPPPKKQDTLMTSRTPETVCVVYDVSHEDPEVKF 60  
**QY** 61 NMVYDGEVHNAVKTPTREEOYNSTYRVVSVLTVLHQNMMNGKEVYCKVSNKALPAPIEKT 120  
 61 NMVYDGEVHNAVKTPTREEOYNSTYRVVSVLTVLHQNMMNGKEVYCKVSNKALPAPIEKT 120  
**DB** 61 NMVYDGEVHNAVKTPTREEOYNSTYRVVSVLTVLHQNMMNGKEVYCKVSNKALPAPIEKT 120  
 61 NMVYDGEVHNAVKTPTREEOYNSTYRVVSVLTVLHQNMMNGKEVYCKVSNKALPAPIEKT 120  
**QY** 121 ISKAKVQPREPOVYTLTPPSRDELTKNOVSLTCLVKGFPYPSDIAVWESNGOPENNYKTTT 180  
 121 ISKAKVQPREPOVYTLTPPSRDELTKNOVSLTCLVKGFPYPSDIAVWESNGOPENNYKTTT 180  
**DB** 121 ISKAKVQPREPOVYTLTPPSRDELTKNOVSLTCLVKGFPYPSDIAVWESNGOPENNYKTTT 180  
 121 ISKAKVQPREPOVYTLTPPSRDELTKNOVSLTCLVKGFPYPSDIAVWESNGOPENNYKTTT 180  
**QY** 181 PVLDSVGSFFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232  
 181 PVLDSGGSFFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYQKSLSLSPGK 232  
**DB** 181 PVLDSGGSFFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYQKSLSLSPGK 232  
 181 PVLDSGGSFFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYQKSLSLSPGK 232

**RESULT 13**  
 US-10-800-449-26  
 : Sequence 26, Application US/10800449  
 : Publication No. US20040265973A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Sun, Lee-Hwei K  
 : APPLICANT: Sun, Bill  
 : APPLICANT: Sun, Cecily R  
 : TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor  
 : TITLE OF INVENTION: increased biological activities  
 : FILE REFERENCE: 03SUN2001  
 : CURRENT APPLICATION NUMBER: US/10/800,449  
 : CURRENT FILING DATE: 2004-03-15  
 : PRIOR APPLICATION NUMBER: US/09/968,362  
 : PRIOR FILING DATE: 2001-10-01  
 : NUMBER OF SEQ ID NOS: 28  
 : SOFTWARE: PatentIn version 3.1  
 : SEQ ID NO 26  
 : LENGTH: 232  
 : TYPE: PRT  
 : ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains  
 US-10-800-449-26

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Query Match      97.2%; Score 1225; DB 16; Length 232;
Best Local Similarity 97.0%; Pred. No. 6,1e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPELLGSPSVFLPPPKPDOTLMIISTPTEVTCVVVDVSHEDPEVKF 60
Db 1 EPKSCDKTHTCPPCPAPELLGSPSVFLPPPKPDOTLMIISTPTEVTCVVVDVSHEDPEVKF 60
QY 61 NWYVDGEVHNNAKTKEPREOYNSTYRVSVLTVLHONMNMNGEKYKKCVSNKALPAPIEKT 120
Db 61 NWYVDGEVHNNAKTKEPREOYNSTYRVSVLTVLHODMWLGKEYKKCVSNKALPAPIEKT 120
QY 121 ISRAKYOPREPQYYTLTPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 121 ISRAKYOPREPQYYTLTPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
QY 124 ISRAKQGPRRPQYYTLTPPSRDELTKNQVSLTCLVKGYFPEDIAVEWESNQGPENNYKTTTP 183
Db 181 PVIIDSGSFPLYSKLTIVDKSRMOOGNVFCSVMHEALHHNYTQKSLSLSPGK 232
Db 181 PVIIDSGSFPLYSKLTIVDKSRMOOGNVFCSVMHEALHHNYTQKSLSLSPGK 232

RESULT 14
US-10-207-655-208
; Sequence 208, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069,401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 208
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion polypeptide
US-10-207-655-208

Query Match      97.2%; Score 1225; DB 14; Length 235;
Best Local Similarity 97.0%; Pred. No. 6,2e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPELLGSPSVFLPPPKPDOTLMIISTPTEVTCVVVDVSHEDPEVKF 60
Db 4 EPKSCDKTHTCPPCPAPELLGSPSVFLPPPKPDOTLMIISTPTEVTCVVVDVSHEDPEVKF 63
QY 61 NWYVDGEVHNNAKTKEPREOYNSTYRVSVLTVLHONMNMNGEKYKKCVSNKALPAPIEKT 120
Db 64 NWYVDGEVHNNAKTKEPREOYNSTYRVSVLTVLHODMWLGKEYKKCVSNKALPAPIEKT 123
QY 121 ISRAKYOPREPQYYTLTPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 124 ISRAKQGPRRPQYYTLTPPSRDELTKNQVSLTCLVKGYFPEDIAVEWESNQGPENNYKTTTP 183
QY 181 PVIIDSGSFPLYSKLTIVDKSRMOOGNVFCSVMHEALHHNYTQKSLSLSPGK 232
Db 184 PVIIDSGSFPLYSKLTIVDKSRMOOGNVFCSVMHEALHHNYTQKSLSLSPGK 235

RESULT 15
US-09-996-357-13
; Sequence 13, Application US/0996357
; Patent No. US20020133001A1
; GENERAL INFORMATION:
; APPLICANT: Gefter, Malcolm L
; APPLICANT: Jereal, David I
; APPLICANT: Joyal, John L
; APPLICANT: Gosseilin, Michael
```

;; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR  
;; TITLE OF INVENTION: TREATING AN AMYLOIDOTIC DISEASE  
;; FILE REFERENCE: PPI-105  
;; CURRENT APPLICATION NUMBER: US/09/996,357  
;; CURRENT FILING DATE: 2001-11-27  
;; PRIOR APPLICATION NUMBER: 60/253,302  
;; PRIOR FILING DATE: 2000-11-27  
;; PRIOR APPLICATION NUMBER: 60/250,198  
;; PRIOR FILING DATE: 2000-11-29  
;; PRIOR APPLICATION NUMBER: 60/257,186  
;; PRIOR FILING DATE: 2000-12-20  
;; NUMBER OF SEQ ID NOS: 13  
;; SOFTWARE: Patentin Ver. 2.0  
;; SEQ ID NO 13  
;; LENGTH: 247  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-996-357-13

Query Match 97.2%; Score 1225; DB 9; Length 247;  
Best Local Similarity 97.0%; Pred. No. 6,6e-90;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKHTHTCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 16 EPKSCDKHTHTCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 75  
QY 61 NMYVDGVEVHNKTRPREQVNSTYRVVSVLTVTHQNMNGKEYCKVSNKALPAPIEKT 120  
DB 76 NMYVDGVEVHNKTRPREQVNSTYRVVSVLTVTHQNMNGKEYCKVSNKALPAPIEKT 135  
QY 121 ISKATVQPREPOVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVWESNNGQPENNYKTT 180  
DB 136 ISKAGQPREPOVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVWESNNGQPENNYKTT 195  
QY 181 PVLDSVGSFELYSLTVDSKRWQGNVFCSYMHEALHNHYOORSLSPGK 232  
DB 196 PVLDSVGSFELYSLTVDSKRWQGNVFCSYMHEALHNHYOORSLSPGK 247

Search completed: June 7, 2005, 09:25:07  
Job time : 102.775 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 08:49:07 ; Search time 32.456 Seconds  
(without alignments)  
533.603 Million cell updates/sec

Title: US-10-000-439-3

Perfect score: 1260

Sequence: 1 EPKSCDKHTHTCPCPAPPELL.....MHEALHNHYQQRSLSPCK 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing:

Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1225	97.2	232	2	US-08-595-043A-50
2	1225	97.2	232	4	US-09-968-362A-26
3	1225	97.2	331	4	US-09-178-869-2
4	1225	97.2	331	4	US-09-761-413-2
5	1225	97.2	360	3	US-09-180-100-11
6	1225	97.2	371	1	US-08-236-311-7
7	1225	97.2	371	4	US-08-457-918-7
8	1225	97.2	371	4	US-10-157-408-7
9	1225	97.2	376	2	US-09-180-100-22
10	1225	97.2	396	2	US-08-784-512-3
11	1225	97.2	424	5	US-09-176-228-3
12	1225	97.2	424	5	PCT-US95-03886-12
13	1225	97.2	424	5	PCT-US85-03886-14
14	1225	97.2	437	5	PCT-US96-10043-11
15	1225	97.2	442	4	US-08-472-888A-7
16	1225	97.2	446	5	PCT-US96-10043-9
17	1225	97.2	449	1	US-08-397-411-7
18	1225	97.2	452	4	US-08-458-516-13
19	1225	97.2	452	4	US-09-773-877B-16
20	1225	97.2	459	1	US-08-157-101A-7
21	1225	97.2	462	4	US-09-773-877B-18
22	1225	97.2	467	4	US-08-030-175-41
23	1225	97.2	467	4	US-08-030-175-42
24	1225	97.2	476	2	US-09-740-002-27
25	1225	97.2	476	2	US-08-378-939-10
26	1225	97.2	476	3	US-08-487-550-4
27	1225	97.2	476	3	US-08-487-550-12

28	1225	97.2	476	4	US-09-526-098-4	Sequence 4, Appl
29	1225	97.2	476	4	US-09-526-098-12	Sequence 12, Appl
30	1225	97.2	476	4	US-09-383-916-4	Sequence 4, Appl
31	1225	97.2	476	3	US-08-487-550-8	Sequence 12, Appl
32	1225	97.2	478	3	US-08-487-550-8	Sequence 8, Appl
33	1225	97.2	478	4	US-09-526-098-8	Sequence 8, Appl
34	1225	97.2	478	4	US-09-383-916-8	Sequence 8, Appl
35	1225	97.2	497	4	US-09-499-846-6	Sequence 6, Appl
36	1225	97.2	525	4	US-09-499-846-4	Sequence 4, Appl
37	1225	97.2	547	4	US-09-746-359A-54	Sequence 54, Appl
38	1225	97.2	557	4	US-09-773-877B-14	Sequence 14, Appl
39	1225	97.2	567	4	US-09-825-561A-16	Sequence 16, Appl
40	1225	97.2	567	4	US-09-773-877B-12	Sequence 12, Appl
41	1225	97.2	567	4	US-09-773-877B-20	Sequence 20, Appl
42	1225	97.2	571	4	US-09-746-359A-53	Sequence 53, Appl
43	1225	97.2	592	4	US-09-313-942-8	Sequence 8, Appl
44	1225	97.2	622	4	US-09-499-846-2	Sequence 2, Appl
45	1225	97.2	859	4	US-09-313-942-7	Sequence 7, Appl

#### ALIGNMENTS

```
RESULT 1
US-08-595-043A-50
; Sequence 50, Application US/08595043A
; Patent No. 5935824
;
; GENERAL INFORMATION:
; APPLICANT: SCARLATO, GREGORY D.
; TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,043A
; FILING DATE: 31-JAN-1996
;
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32, 837
; REFERENCE/DOCKET NUMBER: SGAR-00371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
;
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULAR TYPE: Protein
;
; US-08-595-043A-50
;
; Query Match          97.2%  Score 1225;  DB 2;  Length 232;
; Best Local Similarity 97.0%  Pred. No. 3 6e-116;
; Matches 225;  Conservative 3;  Mismatches 4;  Indels 0;  Gaps 0;
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QY 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLFPKPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 1 EPKSCDKHTHTCPCPAPPELLGSPSVFLFPKPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
QY 61 NMVYDGVENVHAKTKPRERQYNSTYRVSVLTVLHQDNMNGEKYKCKVSNKALPAPIEKT 120  
DB 61 NMVYDGVENVHAKTKPRERQYNSTYRVSVLTVLHQDNMNGEKYKCKVSNKALPAPIEKT 120

QY	QY	QY	QY
122	ISAKXQPEPEPOVYTLPERDELITKNQVSLCTLVAGFAPSPDIAVWESNQGPENNYTTT	121	ISAKXQPEPEPOVYTLPERDELITKNQVSLCTLVAGFAPSPDIAVWESNQGPENNYTTT
121	ISAKXQPEPEPOVYTLPERDELITKNQVSLCTLVAGFAPSPDIAVWESNQGPENNYTTT	120	ISAKXQPEPEPOVYTLPERDELITKNQVSLCTLVAGFAPSPDIAVWESNQGPENNYTTT
181	PVLDISGSGFPLYSKLTVDKSRMQQGNVTSQSYMEALHNHYQQNSLSISPGK	232	PVLDISGSGFPLYSKLTVDKSRMQQGNVTSQSYMEALHNHYQQNSLSISPGK
181	PVLDISGSGFPLYSKLTVDKSRMQQGNVTSQSYMEALHNHYQQNSLSISPGK	232	PVLDISGSGFPLYSKLTVDKSRMQQGNVTSQSYMEALHNHYQQNSLSISPGK

RESULT 2  
US-09-968-362A-26  
; Sequence 26, Application US/09968362A

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? TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
?
? TITLE OF INVENTION: Increased biological activities
?
? FILE REFERENCE: 03SUN2001
?
? CURRENT APPLICATION NUMBER: US/09/968,362A
?
? CURRENT FILING DATE: 2001-10-01
?
? NUMBER OF SEQ ID NOS: 28
?
? SOFTWARE: PatentIn version 3.1
?
? SEQ ID NO 26
?
? LENGTH: 232
?
? TYPE: PRT
?
? ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains
?
? OS-09-968-362A-26

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Query Match	97.2%	Score 1225	DB 4	Length 232
Best Local	97.0%	Pred. No. 3.6e-116		
Matches 225	Conservative	3	Mismatches 4	Indels 0
				Gaps 0

Qy	1	PPKSCDKNHTOPCPAPBELTGGSPVFLPPRKDKDTLMIARTBEVTCVWVDVSHEDBEVXF	60
Qy	1	PPKSCDKNHTOPCPAPBELTGGSPVFLPPRKDKDTLMIARTBEVTCVWVDVSHEDBEVXF	60
Db	1	EPKSCDKHTOPCPAPBELTGGSPVFLPPRKDKDTLMIARTBEVTCVWVDVSHEDBEVXF	60
Qy	61	NMYVDGVEVHNVTKTRREBOYNSTYRVVSVLTVLHQNMMNGKXEYCKKCVSNKALPAPIEKT	120
Db	61	NMYVDGVEVHNVTKTRREBOYNSTYRVVSVLTVLHQNMMNGKXEYCKKCVSNKALPAPIEKT	120
Qy	121	ISKAKVOPREPOVYTLPPSRDELTAKQVSLTCLVKGFIYSDIAVEMESNGOPENNYKTTT	180
Db	121	ISKAKGOREPOVYTLPPSRDELTAKQVSLTCLVKGFIYSDIAVEMESNGOPENNYKTTT	180
Qy	181	PVLDVSQGFPLYSKLTVDKSRWQOQNVPSCSVMHEALHNNHYQOORSLSLSPGK	232
Db	181	PVLDSDGSEFLYSKLTVDKSRWQOQNVPSCSVMHEALHNNHYQOORSLSLSPGK	232

RESULT 3  
US-09-178-869-2  
; Sequence 2, Application US/09178869B  
; Patent No. 6197294

GENERAL INFORMATION:  
APPLICANT: Tao, Weng  
APPLICANT: Wong, Shou  
APPLICANT: Hickey, William F.  
APPLICANT: Hamman, Joseph P.  
APPLICANT: Baetge, E. Edward  
TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION  
FILE REFERENCE: 17810-043  
CURRENT APPLICATION NUMBER: US/09/178,869S  
CURRENT FILING DATE: 1998-10-26  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-178-869-2

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Query Match	97.2%;	Score 1225;	DB 3;	Length 331;
Best Local Similarity	97.0%;	Pred. No. 6,1e-116;		
Matches 225;	Conservative 3;	Mismatches 4;	Indels 0;	Gaps 0;

Qy	1	EPKSCNKHTCPPCAPBELLGSPSFLFPPKPKDTLMI	SRPPELTCTVVDVSHDEBVKF	60
Db	100	EPKSCNKHTCPPCAPBELLGSPSFLFPPKPKDTLMI	SRPPELTCTVVDVSHDEBVKF	159
Qy	61	NWYVDGEVHNHNYKTRPREEQYNSTRVVS	YLTVLHQMNMNGKEYCKCYVSNKALPAPLEKT	120
Db	160	NWYVDGEVHNHNYKTRPREEQYNSTRVVS	YLTVLHQMNMNGKEYCKCYVSNKALPAPLEKT	219
Qy	121	ISFAKVQPREPOVYTYLPSPRDELTJKNQVSLTCLV	KGFPSPDIAMWESNQGPENNYKTTIP	160
Db	220	ISFAKVQPREPOVYTYLPSPRDELTJKNQVSLTCLV	KGFPSPDIAMWESNQGPENNYKTTIP	279
Qy	181	PVLDSDGSFFLYSKLTVDSKRWQGNVSSCSVMHEALH	NHNYQGNLSLSLSPGK	232
Db	280	PVLDSDGSFFLYSKLTVDSKRWQGNVSSCSVMHEALH	NHNYQGNLSLSLSPGK	331

RESULT 4  
US-09-761-413-2

```

1      Sequence 2, Application US/09761413
2      Patent No. 6506891
3      GENERAL INFORMATION:
4      APPLICANT: Tao, Weng
5      APPLICANT: Wong, Shou
6      APPLICANT: Hickey, William F.
7      APPLICANT: Hamann, Joseph P.
8      APPLICANT: Baetge, E. Edward
9      TITLE OF INVENTION: CELL SURFACE-INDUCED
10     FILE REFERENCE: 17810-043
11     CURRENT APPLICATION NUMBER: US/09/761,413
12     CURRENT FILING DATE: 2001-01-16
13     PRIOR APPLICATION NUMBER: US/09/178,869
14     PRIOR FILING DATE: 1998-10-26
15     NUMBER OF SEQ ID NOS: 14
16     SOFTWARE: PatentIn Ver. 2.0
17     SEQ ID NO 2
18     LENGTH: 331
19     TYPE: PRT
20     ORGANISM: Homo sapiens
21     US-09-761-413-2

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Query Match	97.2%	Score 1225;	DB 4;	Length 331;
Best Local Similarity	97.0%	Pred. No. 6.1e-116;		
Matches 225; Conservative	3;	Mismatches 4;	Indels 0;	Gaps 0.

Qy	1	EPKSCDKHTCPPCAPPELLGGPSVFLPPLPKDTLMISRTPELTCCVVDVSHEDPEVK	60
Db	100	EPKSCDKHTCPPCAPPELLGGPSVFLPPLPKDTLMISRTPELTCCVVDVSHEDPEVK	159
Qy	61	NMYVDGEVHNHYKTRKEEQYNSTRVSVLTVLHQNMNNGKEYCKCYSNKALPAPIEKT	120
Db	160	NMYVDGEVHNHYKTRKEEQYNSTRVSVLTVLHQNMNNGKEYCKCYSNKALPAPIEKT	219
Qy	121	ISKAKYQPREPQVYTLPPSRDELITKNQVSLTCLVKGFPSDIAVWESNCGPENNYYKTP	180
Db	220	ISKAKYQPREPQVYTLPPSRDELITKNQVSLTCLVKGFPSDIAVWESNCGPENNYYKTP	279
Qy	181	PVLDISGSPFLYSKLTVDKSRWQOGNVSCSYMHGALHNHYTQSSLSLRPK	232
Db	280	PVLDISGSPFLYSKLTVDKSRWQOGNVSCSYMHGALHNHYTQSSLSLRPK	331

## RESULT 5

US-09-180-100-11  
; Sequence 11, Application US/09180100  
; Patent No. 6306395  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, No. 630639510

APPLICANT: NAGATA, Shigekazu  
TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE  
FILE REFERENCE: 1110-207P  
CURRENT APPLICATION NUMBER: US/09/180,100  
CURRENT FILING DATE: 1998-11-02  
EARLIER APPLICATION NUMBER: PCT/JP97/01502  
EARLIER FILING DATE: 1997-05-01  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 11  
LENGTH: 360  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-180-100-11

Query Match 97.2% Score 1225; DB 3; Length 360;  
Best Local Similarity 97.0%; Pred. No. 6,9e-116;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 BEKSCDKHTHCPCPAPBLGGPSVFLPFPKPKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
DB 129 BEKSCDKHTHCPCPAPBLGGPSVFLPFPKPKDTLMSRTPEVTCVVVDVSHEDPEVKF 188  
DB 189 NMVYDGEVHNKTPREEQYNSTRVVSVLTVLHQMNGEKYCKYSNKKLLPAPIEKT 248  
QY 121 ISKAVQPREPOVYTLPSRDELTKNOVSLTCLVGFPSDIAVEMESGOPENNYKTP 180  
DB 249 ISKAGQPREPOVYTLPSRDELTKNOVSLTCLVGFPSDIAVEMESGOPENNYKTP 308  
QY 181 PVLDSGSEFLYSKLTVDKSRWQGNVFSQVMHEALHNHYOQRSLSLSPGK 232  
DB 309 PVLDSGSEFLYSKLTVDKSRWQGNVFSQVMHEALHNHYOQRSLSLSPGK 360

## RESULT 6

US-08-236-311-7  
Sequence 7, Application US/08236311  
Patent No. 5565335  
GENERAL INFORMATION:  
APPLICANT: Capon, Daniel J.  
APPLICANT: Gregory, Timothy J.  
TITLE OF INVENTION: Adhesion Variants  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/236,311  
FILING DATE: 02-MAY-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/936190  
FILING DATE: 26-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/842777  
FILING DATE: 18-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/250785  
FILING DATE: 28-SEP-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/104329  
FILING DATE: 02-OCT-1987

ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 444PIC2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 371 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-236-311-7

Query Match 97.2% Score 1225; DB 1; Length 371;  
Best Local Similarity 97.0%; Pred. No. 7,2e-116;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 BEKSCDKHTHCPCPAPBLGGPSVFLPFPKPKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
DB 140 BEKSCDKHTHCPCPAPBLGGPSVFLPFPKPKDTLMSRTPEVTCVVVDVSHEDPEVKF 199  
DB 200 NMVYDGEVHNKTPREEQYNSTRVVSVLTVLHQMNGEKYCKYSNKKLLPAPIEKT 259  
QY 121 ISKAVQPREPOVYTLPSRDELTKNOVSLTCLVGFPSDIAVEMESGOPENNYKTP 180  
DB 260 ISKAGQPREPOVYTLPSRDELTKNOVSLTCLVGFPSDIAVEMESGOPENNYKTP 319  
QY 181 PVLDSGSEFLYSKLTVDKSRWQGNVFSQVMHEALHNHYOQRSLSLSPGK 232  
DB 320 PVLDSGSEFLYSKLTVDKSRWQGNVFSQVMHEALHNHYOQRSLSLSPGK 371

## RESULT 7

US-08-457-918-7  
Sequence 7, Application US/08457918  
Patent No. 6117655  
GENERAL INFORMATION:  
APPLICANT: Capon, Daniel J.  
APPLICANT: Gregory, Timothy J.  
TITLE OF INVENTION: Adhesion Variants  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/457,918  
FILING DATE: 1-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/236311  
FILING DATE: 02-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/936190  
FILING DATE: 26-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/842777  
FILING DATE: 18-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/250785  
FILING DATE: 28-SEP-1988

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/104329  
FILING DATE: 02-OCT-1987  
ATTORNEY/AGENT INFORMATION:  
NAME: Kubinec, Jeffrey S.  
REGISTRATION NUMBER: 36,575  
REFERENCE/DOCKET NUMBER: P0444P1C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8228  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 371 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-457-918-7

Query Match 97.2%; Score 1225; DB 3; Length 371;  
Best Local Similarity 97.0%; Pred. No. 7.2e-116;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPBLGSPVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
DB 140 EPKSCDKHTHTCPCPAPBLGSPVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 199  
QY 61 NMVYDGEVHVNKTKRREQYNSTYRVSVLTVLIHQNMNGEKYCKVSNKALPAPIEKT 120  
DB 200 NMVYDGEVHVNKTKRREQYNSTYRVSVLTVLIHQDMINGEKYCKVSNKALPAPIEKT 259  
QY 121 ISKAVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 180  
DB 260 ISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 319  
QY 181 PVLDSVGSFFLYSLKLTVDKSRWQGNVSPCSYMHKALHNHYQKLSLSPGK 232  
DB 320 PVLDSVGSFFLYSLKLTVDKSRWQGNVSPCSYMHKALHNHYQKLSLSPGK 371

RESULT 8  
US-10-157-408-7  
Sequence 7, Application US/10157408  
Patent No. 6710169  
GENERAL INFORMATION:  
APPLICANT: Capon, Daniel J.  
Gregory, Timothy J.  
TITLE OF INVENTION: Adhesion Variants  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/157,408  
FILING DATE: 28-May-2002  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/457,918  
FILING DATE: 1-JUN-1995  
APPLICATION NUMBER: 08/236311  
FILING DATE: 02-MAY-1994  
APPLICATION NUMBER: 07/936190  
FILING DATE: 26-AUG-1992  
APPLICATION NUMBER: 07/842777  
FILING DATE: 18-FEB-1992

APPLICATION NUMBER: 07/250785  
FILING DATE: 28-SEP-1988  
APPLICATION NUMBER: 07/104329  
FILING DATE: 02-OCT-1987  
ATTORNEY/AGENT INFORMATION:  
NAME: Kubinec, Jeffrey S.  
REGISTRATION NUMBER: 36,575  
REFERENCE/DOCKET NUMBER: P0444P1C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8228  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 371 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-157-408-7

Query Match 97.2%; Score 1225; DB 4; Length 371;  
Best Local Similarity 97.0%; Pred. No. 7.2e-116;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPBLGSPVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
DB 140 EPKSCDKHTHTCPCPAPBLGSPVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 199  
QY 61 NMVYDGEVHVNKTKRREQYNSTYRVSVLTVLIHQNMNGEKYCKVSNKALPAPIEKT 120  
DB 200 NMVYDGEVHVNKTKRREQYNSTYRVSVLTVLIHQDMINGEKYCKVSNKALPAPIEKT 259  
QY 121 ISKAVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 180  
DB 260 ISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 319  
QY 181 PVLDSVGSFFLYSLKLTVDKSRWQGNVSPCSYMHKALHNHYQKLSLSPGK 232  
DB 320 PVLDSVGSFFLYSLKLTVDKSRWQGNVSPCSYMHKALHNHYQKLSLSPGK 371

RESULT 9  
US-09-180-100-22  
Sequence 22, Application US/09180100  
Patent No. 6306395  
GENERAL INFORMATION:  
APPLICANT: NAKAMURA, No. 6306395  
FILE REFERENCE: 1110-207P  
TITLE OF INVENTION: NOVEL Ras ANTIGEN DERIVATIVE  
CURRENT APPLICATION NUMBER: US/09/180,100  
CURRENT FILING DATE: 1998-11-02  
EARLIER APPLICATION NUMBER: PCT/JP97/01502  
EARLIER FILING DATE: 1997-05-01  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 22  
LENGTH: 376  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-180-100-22

Query Match 97.2%; Score 1225; DB 3; Length 376;  
Best Local Similarity 97.0%; Pred. No. 7.3e-116;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPBLGSPVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
DB 145 EPKSCDKHTHTCPCPAPBLGSPVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 204  
QY 61 NMVYDGEVHVNKTKRREQYNSTYRVSVLTVLIHQNMNGEKYCKVSNKALPAPIEKT 120  
DB 205 NMVYDGEVHVNKTKRREQYNSTYRVSVLTVLIHQDMINGEKYCKVSNKALPAPIEKT 264

QY 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGOPENNYKTP 180  
| | | | |  
DB 265 ISKAGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGOPENNYKTP 324  
| | | | |  
QY 181 PVLDSVGSFELYSKLTVDKSRWQGNVFSQVMEALHNHYOORSLSLSPGK 232  
| | | | |  
DB 345 PVLDSVGSFELYSKLTVDKSRWQGNVFSQVMEALHNHYOORSLSLSPGK 376  
| | | | |

## RESULT 10

US-08-784-512-3  
; Sequence 3, Application US/08784512  
; Patent No. 5872209  
; GENERAL INFORMATION:  
; APPLICANT: BARTNIK, Eckart  
; APPLICANT: EIDENMUELLER, Bernd  
; APPLICANT: BUETTNER, Frank  
; APPLICANT: CATERSON, Bruce  
; APPLICANT: HUGHES, Clare  
; TITLE OF INVENTION: An artificial recombinant substrate (RAGG 1)  
; TITLE OF INVENTION: and native aggreacan to study the proteolytic activity of  
; TITLE OF INVENTION: "Aggreacanase" in cell culture systems  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Foley & Lardner  
; STREET: Suite 500, 3000 K Street, N.W.  
; CITY: Washington, D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/784,512  
; FILING DATE: 17-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: BP 96100682.2  
; FILING DATE: 18-JAN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GRANADOS, Patricia D.  
; REGISTRATION NUMBER: 33,683  
; REFERENCE/DOCKET NUMBER: 18748/311  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 672-5300  
; TELEFAX: (202) 672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 396 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..396  
; US-08-784-512-3

Query Match 97.2%; Score 1225; DB 2; Length 396;

Best Local Similarity 97.0%; Pred. No. 7, 9e-116; Indels 0; Gaps 0;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPBLIGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
| | | | |  
DB 165 EPKSCDKHTHTCPCPAPBLIGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 224  
| | | | |  
QY 61 NMYVDGVEVHNAKTRPREQYNSTYRVVSVLTVLHQDNMNGEKYKCKVSNKALPAPIEKT 120  
| | | | |  
DB 225 NMYVDGVEVHNAKTRPREQYNSTYRVVSVLTVLHQDNMNGEKYKCKVSNKALPAPIEKT 284  
| | | | |

QY 121 ISKAVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGOPENNYKTP 180  
| | | | |  
DB 265 ISKAGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGOPENNYKTP 344  
| | | | |  
QY 181 PVLDSVGSFELYSKLTVDKSRWQGNVFSQVMEALHNHYOORSLSLSPGK 232  
| | | | |  
DB 345 PVLDSVGSFELYSKLTVDKSRWQGNVFSQVMEALHNHYOORSLSLSPGK 396  
| | | | |

## RESULT 11

US-09-176-228-3  
; Sequence 3, Application US/09176228  
; Patent No. 6180334  
; GENERAL INFORMATION:  
; APPLICANT: BARTNIK, Eckart  
; APPLICANT: EIDENMUELLER, Bernd  
; APPLICANT: BUETTNER, Frank  
; APPLICANT: CATERSON, Bruce  
; APPLICANT: HUGHES, Clare  
; TITLE OF INVENTION: An artificial recombinant substrate (RAGG 1)  
; TITLE OF INVENTION: and native aggreacan to study the proteolytic activity of  
; TITLE OF INVENTION: "Aggreacanase" in cell culture systems  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Foley & Lardner  
; STREET: Suite 500, 3000 K Street, N.W.  
; CITY: Washington, D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/176,228  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/784,512  
; FILING DATE: 17-JAN-1997  
; APPLICATION NUMBER: BP 96100682.2  
; FILING DATE: 18-JAN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GRANADOS, Patricia D.  
; REGISTRATION NUMBER: 33,683  
; REFERENCE/DOCKET NUMBER: 18748/311  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 672-5300  
; TELEFAX: (202) 672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 396 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..396  
; US-09-176-228-3

Query Match 97.2%; Score 1225; DB 3; Length 396;

Best Local Similarity 97.0%; Pred. No. 7, 9e-116; Indels 0; Gaps 0;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPBLIGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
| | | | |  
DB 165 EPKSCDKHTHTCPCPAPBLIGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 224  
| | | | |  
QY 61 NMYVDGVEVHNAKTRPREQYNSTYRVVSVLTVLHQDNMNGEKYKCKVSNKALPAPIEKT 120  
| | | | |  
DB 225 NMYVDGVEVHNAKTRPREQYNSTYRVVSVLTVLHQDNMNGEKYKCKVSNKALPAPIEKT 284  
| | | | |

QY 121 ISKAVQPREPOVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVWESNGOPENNYKTTT 180  
| | | | |  
DB 285 ISKAGQPREPOVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVWESNGOPENNYKTTT 344  
| | | | |  
QY 181 PVLDSGSEFLYSKLTVDKSRMOQGNVSCSVMEHALHNHYOQRSLSLSPGK 232  
| | | | |  
DB 345 PVLDSGSEFLYSKLTVDKSRMOQGNVSCSVMEHALHNHYOQRSLSLSPGK 396  
| | | | |  
RESULT 12  
PCT-US95-03866-12  
; Sequence 12, Application PC/TUS9503866  
; GENERAL INFORMATION:  
; APPLICANT: Cycomed, Inc. (all states except US)  
; APPLICANT: Nocka, Karl (US only)  
; APPLICANT: Lobell, Robert B (US only)  
; TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND  
; TITLE OF INVENTION: FLT-3/FLK-2 LIGAND  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/03866  
; FILING DATE:  
; CLASSIFICATION:  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/220,379  
; FILING DATE: 28-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr, James F  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: Cycomed/2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-596-9090  
; TELEFAX: 212-596-9000  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 424 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US95-03866-12  
Query Match 97.2%; Score 1225; DB 5; Length 424;  
Best Local Similarity 97.0%; Pred. No. 8.7e-116;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKHTHTCPCPAPBLGSPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
| | | | |  
DB 193 EPKSCDKHTHTCPCPAPBLGSPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 252  
| | | | |  
QY 61 NWYDVGVEVHNAKTPREBOYNSTRVYVSLTVLHQNMNGKEYCKYSNKAALPAPIEKT 120  
| | | | |  
DB 253 NWYDVGVEVHNAKTPREBOYNSTRVYVSLTVLHQNMNGKEYCKYSNKAALPAPIEKT 312  
| | | | |  
QY 121 ISKAVQPREPOVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVWESNGOPENNYKTTT 180  
| | | | |  
DB 313 ISKAGQPREPOVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVWESNGOPENNYKTTT 372  
| | | | |  
QY 181 PVLDSGSEFLYSKLTVDKSRMOQGNVSCSVMEHALHNHYOQRSLSLSPGK 232  
| | | | |  
DB 373 PVLDSGSEFLYSKLTVDKSRMOQGNVSCSVMEHALHNHYOQRSLSLSPGK 424  
| | | | |

RESULT 13  
PCT-US95-03866-14  
; Sequence 14, Application PC/TUS9503866  
; GENERAL INFORMATION:  
; APPLICANT: Cycomed, Inc. (all states except US)  
; APPLICANT: Nocka, Karl (US only)  
; APPLICANT: Lobell, Robert B (US only)  
; TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND  
; TITLE OF INVENTION: FLT-3/FLK-2 LIGAND  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/03866  
; FILING DATE:  
; CLASSIFICATION:  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/220,379  
; FILING DATE: 28-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr, James F  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: Cycomed/2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-596-9090  
; TELEFAX: 212-596-9000  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 424 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US95-03866-14  
Query Match 97.2%; Score 1225; DB 5; Length 424;  
Best Local Similarity 97.0%; Pred. No. 8.7e-116;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKHTHTCPCPAPBLGSPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 60  
| | | | |  
DB 193 EPKSCDKHTHTCPCPAPBLGSPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKF 252  
| | | | |  
QY 61 NWYDVGVEVHNAKTPREBOYNSTRVYVSLTVLHQNMNGKEYCKYSNKAALPAPIEKT 120  
| | | | |  
DB 253 NWYDVGVEVHNAKTPREBOYNSTRVYVSLTVLHQNMNGKEYCKYSNKAALPAPIEKT 312  
| | | | |  
QY 121 ISKAVQPREPOVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVWESNGOPENNYKTTT 180  
| | | | |  
DB 313 ISKAGQPREPOVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVWESNGOPENNYKTTT 372  
| | | | |  
QY 181 PVLDSGSEFLYSKLTVDKSRMOQGNVSCSVMEHALHNHYOQRSLSLSPGK 232  
| | | | |  
DB 373 PVLDSGSEFLYSKLTVDKSRMOQGNVSCSVMEHALHNHYOQRSLSLSPGK 424  
| | | | |  
RESULT 14  
PCT-US96-10043-11  
; Sequence 11, Application PC/TUS9610043  
; GENERAL INFORMATION:  
; APPLICANT: The General Hospital Corporation  
; TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES



```

; TITLE OF INVENTION: AND METHODS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10043
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,213
; FILING DATE: 14-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lech, Karen P.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 00786/284001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-10043-11

Query Match          97.2%; Score 1225; DB 5; Length 437;
Best Local Similarity 97.0%; Pred. No. 9.1e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPELLGSPSVFLPPPKKDTLMISRTPEVTCVVDVSHDEPEVKF 60
DB 206 EPKSCDKHTHTCPCPAPELLGSPSVFLPPPKKDTLMISRTPEVTCVVDVSHDEPEVKF 265
QY 61 NMYVDGVEVHNAVTKYKREBOYNSTYRVSVLTVLHONMNGEKYCKKVSNNKALPAPIEKT 120
DB 266 NMYVDGVEVHNAVTKYKREBOYNSTYRVSVLTVLHODMNGEKYCKKVSNNKALPAPIEKT 325
QY 121 ISKAVQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGOPENNYKTTTP 180
DB 326 ISKAGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGOPENNYKTTTP 385
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVMHBALNHHYQORSLSLSPGK 232
DB 386 PVLDSGGSFFLYSKLTVDKSRWQGNVFCSVMHBALNHHYQORSLSLSPGK 437

RESULT 15
US-08-472-888A-7
; Sequence 7, Application US/08472888A
; Patent No. 6613746
; GENERAL INFORMATION:
; APPLICANT: Seed, Brian
; APPLICANT: Walz, Gerd
; TITLE OF INVENTION: AGP-ANTIBODY FUSION PROTEINS
; TITLE OF INVENTION: AND RELATED MOLECULES AND METHODS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
```

```

; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,888A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/618,314
; FILING DATE: 23-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Elbing, Karen L.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/258001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 442 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-472-888A-7
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Query Match          97.2%; Score 1225; DB 4; Length 442;
Best Local Similarity 97.0%; Pred. No. 9.3e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPELLGSPSVFLPPPKKDTLMISRTPEVTCVVDVSHDEPEVKF 60
DB 211 EPKSCDKHTHTCPCPAPELLGSPSVFLPPPKKDTLMISRTPEVTCVVDVSHDEPEVKF 270
QY 61 NMYVDGVEVHNAVTKYKREBOYNSTYRVSVLTVLHONMNGEKYCKKVSNNKALPAPIEKT 120
DB 271 NMYVDGVEVHNAVTKYKREBOYNSTYRVSVLTVLHODMNGEKYCKKVSNNKALPAPIEKT 330
QY 121 ISKAVQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGOPENNYKTTTP 180
DB 331 ISKAGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGOPENNYKTTTP 390
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSVMHBALNHHYQORSLSLSPGK 232
DB 391 PVLDSGGSFFLYSKLTVDKSRWQGNVFCSVMHBALNHHYQORSLSLSPGK 442
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Search completed: June 7, 2005, 09:04:01  
Job time : 33.456 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 08:48:08 ; Search time 1.79102 Seconds  
(without alignments)  
913.271 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94

Sequence: 1 ENPVVHFFKNIVTPRTP 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	100.0	128	1 MBRTS	myelin basic prote
2	94	100.0	167	2 A37246	myelin basic prote
3	94	100.0	169	1 MBROB	myelin basic prote
4	94	100.0	171	1 MBCEB	myelin basic prote
5	94	100.0	171	1 MBPGB	myelin basic prote
6	94	100.0	197	1 MBHUB	myelin basic prote
7	94	100.0	328	1 MBMSB	goli-myelin basic
8	87	92.6	174	2 S08535	myelin basic prote
9	60	63.8	128	2 A60215	myelin basic prote
10	53	56.4	155	2 B32959	myelin basic prote
11	45	47.9	308	2 G64440	hypothetical prote
12	44	46.8	329	2 A57246	beta-lectorin prec
13	44	45.8	639	2 T46577	arylsulfatase (BC
14	43	45.7	14	2 S12804	protein kinase (BC
15	43	45.7	85	2 C89965	conserved hypothet
16	43	45.7	134	2 T28704	hypothetical prote
17	43	45.7	395	2 H72222	conserved hypothet
18	43	45.7	672	2 A11183	transcription regu
19	43	45.7	1124	2 B84742	probable receptor-
20	42	44.7	435	2 AB3076	glutamine synthet
21	42	44.7	435	2 G98210	glutamine synthet
22	42	44.7	435	2 JC1301	glutamate-ammonia
23	42	44.7	672	2 AG1541	similar to transcr
24	42	44.7	891	2 T40137	hypothetical serin
25	41	43.6	48	2 D82534	hypothetical prote
26	41	43.6	332	2 E70384	biotin synthase (E
27	41	43.6	480	2 A12308	cytochrome D ubiqu
28	41	43.6	646	2 A11174	internalin, probab
29	41	43.6	690	2 E84945	glycine-tRNA ligas

30	41	43.6	892	2 T27005	hypothetical prote
31	40	42.6	192	2 AD2530	hypothetical prote
32	40	42.6	428	2 D96934	cytosine/guanine d
33	40	42.6	431	2 T50177	probable peptide m
34	40	42.6	983	2 H72510	probable ribonucle
35	40	42.6	1162	2 T51040	hypothetical prote
36	40	42.6	2089	2 C85426	ATM-like protein (
37	40	42.6	3738	2 T05501	hypothetical prote
38	39	41.5	164	2 F88690	protein F41H10.2 (
39	39	41.5	250	2 B81262	glutamate racemase
40	39	41.5	270	2 F86897	hypothetical prote
41	39	41.5	323	2 T15311	hypothetical prote
42	39	41.5	333	2 S18578	C4-dicarboxylate-b
43	39	41.5	337	2 F89944	conserved hypothet
44	39	41.5	431	2 H70302	conserved hypothet
45	39	41.5	471	2 AB0308	o-succinylbenzoate

## ALIGNMENTS

## RESULT 1

MBRTS

myelin basic protein S - rat  
N/Alternate names: small myelin basic protein

C/Species: Rattus norvegicus (Norway rat)

C/Date: 24-Apr-1984 #sequence revision 08-Feb-1996 #ext\_change 09-Jul-2004

C/Accession: B24351; A90275; A94243; A21062; A03142

R/Schach, M.; Budzinski, R.M.; Stoffel, W.

Biol. Chem. Hoppe-Seyler 367, 825-834, 1986

A/Title: Cloned proteolipid protein and myelin basic protein cDNA. Transcription of the t

A/Reference number: A24351; UID:87026249; PMID:2429678

A/Accession: B24351

A/Molecule type: mRNA

A/Residues: 1-128 <SCH>

A/Cross-references: UNIPROT:P02668; EMBL:M25889; NID:G205321; PIDN:AAA41575.1; PID:G20532

R/Dunkley, P.R.; Carnegie, P.R.

Biochem. J. 141, 243-255, 1974

A/Title: Amino acid sequence of the smaller basic protein from rat brain myelin.

A/Reference number: A90275; UID:75127359; PMID:4141893

A/Accession: A90275

A/Molecule type: protein

A/Residues: 2-128 <DUN>

A/Note: at position 105, arginine, monomethylarginine, and dimethylarginine occur in the

A/Note: rats have two myelin basic proteins; the smaller one, shown above, is missing 40

R/McFarlin, D.E.; Blank, S.E.; Kibler, R.F.; McKeally, S.; Shapira, R.

Science 179, 478-480, 1973

A/Title: Experimental allergic encephalomyelitis in the rat: response to encephalitogenic

A/Reference number: A94243; UID:73180720; PMID:4122324

A/Accession: A94243

A/Molecule type: protein

A/Residues: 46-86 <MCF>

A/Note: the sequence reported for this encephalitogenic peptide differs from that shown i

R/Boach, A.; Boylan, K.; Horvath, S.; Prusiner, S.B.; Hood, L.B.

Cell 34, 799-806, 1983

A/Title: Characterization of cloned cDNA representing rat myelin basic protein: absence c

A/Reference number: A21062; UID:84026484; PMID:6194889

A/Accession: A21062

A/Molecule type: mRNA

A/Residues: 1-124, 126-128 <ROA>

A/Experimental source: strain Sprague-Dawley

C/Suprafamily: myelin basic protein

C/Keywords: alternative splicing; blocked amino end; experimental autoimmune encephalomy

F/2-128/Product: myelin basic protein S #status experimental <MAT>

F/2/Modified site: blocked amino end (Ala) (in mature form) (probably acetylated) #statu

F/105/Modified site: omega-N-methylarginine or omega-N'-methylarginine (Arg) (if

Query Match 100.0%; Score 94; DB 1; Length 128;

Best local similarity 100.0%; Pred. No. 1e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
|||||

Db 81 ENPVVHFFKNIVTPRTP 97

RESULT 2

A37246

myelin basic protein - guinea pig

N:Alternate names: myelin A1 protein

C:Species: Cavia porcellus (guinea pig)

C:Date: 31-Jul-1991 #sequence\_revision 31-Jul-1991 #ext\_change 09-Jul-2004

C:Accession: A37246; C92087; A03140

R:Deblater, G.E.; Martenson, R.E.; Krutzsch, H.C.; Kies, M.W.

J. Neurochem. 43, 100-105, 1984

A:Title: Sequence of guinea pig myelin basic protein.

A:Reference number: A37246; PMID:84215086; PMID:6202840

A:Accession: A37246

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-167 <DEI>

A:Cross-references: UNIPROT:P25188

R:Shapiro, R.; McKneally, S.S.; Chou, F.; Kibler, R.F.

U. Biol. Chem. 246, 4630-4640, 1971

A:Title: Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovin

A:Reference number: A92087

A:Accession: C92087

A:Molecule type: protein

A:Residues: 45-87 <SHA>

C:Superfamily: myelin basic protein

C:Keywords: myelin

Query Match 100.0%; Score 94; DB 2; Length 167;  
Best Local Similarity 100.0%; Pred. No. 1.4e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVHFFKNIVTPRTP 17  
|||||

Db 82 ENPVVHFFKNIVTPRTP 98

RESULT 3

MEBOB

myelin basic protein - bovine

N:Alternate names: myelin A1 protein

C:Species: Bos primigenius taurus (cattle)

C:Date: 18-Dec-1981 #sequence\_revision 18-Dec-1981 #ext\_change 09-Jul-2004

C:Accession: A92089; A92160; A92087; S54343; A61641; B61641; A03140

R:Eylar, E.H.; Brostoff, S.; Hashim, G.; Caccam, J.; Burnett, P.

J. Biol. Chem. 246, 5770-5784, 1971

A:Title: Basic A1 protein of the myelin membrane. The complete amino acid sequence.

A:Reference number: A92089; PMID:72007306; PMID:5096093

A:Accession: A92089

A:Molecule type: protein

A:Residues: 1,'S',2-169 <EXL>

A:Cross-references: UNIPROT:P02687

R:Brostoff, S.W.; Reuter, W.; Hichens, M.; Eylar, E.H.

U. Biol. Chem. 249, 558-567, 1974

A:Title: Specific cleavage of the A1 protein from myelin with cathepsin D.

A:Reference number: A92160; PMID:74070688; PMID:4129204

A:Accession: A92160

A:Molecule type: protein

A:Residues: 1-169 <BRO>

R:Shapiro, R.; McKneally, S.S.; Chou, F.; Kibler, R.F.

U. Biol. Chem. 246, 4630-4640, 1971

A:Title: Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovin

A:Reference number: A92087

A:Accession: A92087

A:Molecule type: protein

A:Residues: 43-87 <SHA>

R:Okazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.

Biochem. J. 306, 551-555, 1995

A:Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in glia

A:Reference number: S54343; PMID:95194333; PMID:7687910

A:Accession: S54343

A:Molecule type: protein

A:Residues: 74-75,'HG',78-82,'D',84-88,105,'X',107-108,'X',110-114,'X',116-119 <OKA>

R:Takamatsu, K.; Iatencio, K.

Neurochem. Res. 17, 239-246, 1992

A:Title: Isolation and characterization of two novel peptide amides originating from myel

A:Reference number: A61641; PMID:92319189; PMID:1377792

A:Accession: A61641

A:Molecule type: protein

A:Residues: 1-112 <TKA>

A:Accession: B61641

A:Molecule type: protein

A:Residues: 1-16 <TA2>

A:Note: these peptides have carboxyl-terminal amides probably produced by a non-enzymatic

R:Brostoff, S.; Eylar, E.H.

Proc. Natl. Acad. Sci. U.S.A. 68, 765-769, 1971

A:Title: Localization of methylated arginine in the A1 protein from myelin.

A:Reference number: A93777; PMID:71153946; PMID:4994464

A:Contents: annotation

A:Note: Arg-106 is modified to monomethylarginine and dimethylarginine

R:Eylar, E.H.; Caccam, J.; Jackson, J.J.; Westall, F.C.; Robinson, A.B.

Science 168, 1220-1223, 1970

A:Title: Experimental allergic encephalomyelitis: synthesis of disease-inducing site of t

A:Reference number: A94241; PMID:70178977; PMID:5442707

A:Contents: annotation

A:Note: the region including residues 114-122 induces experimental allergic encephalomyel

C:Superfamily: myelin basic protein

C:Keywords: acetylated amino end; amidated carboxyl end; experimental autoimmune encephal

F:1-169/Product: myelin basic protein #status experimental <MAT>

F:1-16/Product: myelin peptide amide-16 #status experimental <PAL6>

F:1-12/Product: myelin peptide amide-12 #status experimental <PAL2>

F:12/Modified site: acetylated amino end (Ala) #status experimental

F:16/Modified site: amidated carboxyl end (Tyr) (amide in mature form myelin peptide amic

F:16/Modified site: amidated carboxyl end (Ala) (amide in mature form myelin peptide amic

F:106/Modified site: omega-N-methylarginine or omega-N-dimethylarginine (Arg) (i

Query Match 100.0%; Score 94; DB 1; Length 169;  
Best Local Similarity 100.0%; Pred. No. 1.4e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVHFFKNIVTPRTP 17  
|||||

Db 82 ENPVVHFFKNIVTPRTP 98

RESULT 4

MBC2B

myelin basic protein - chimpanzee (tentative sequence)

N:Alternate names: MBP

C:Species: Pan troglodytes (chimpanzee)

C:Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #ext\_change 09-Jul-2004

C:Accession: A03139

R:Westall, F.C.; Thompson, M.; Kalter, S.S.

Life Sci. 17, 219-223, 1975

A:Title: The proposed sequence of the encephalitogenic protein from chimpanzee brain.

A:Reference number: A03139; PMID:76009821; PMID:51459

A:Accession: A03139

A:Molecule type: protein

A:Residues: 1-171 <WES>

A:Cross-references: UNIPROT:P06906

C:Comment: This protein may function in maintaining the proper structure of myelin.

C:Superfamily: myelin basic protein

C:Keywords: blocked amino end; methylated amino acid; myelin; structural protein

F:1/Modified site: blocked amino end (Ala) (probably acetylated) #status experimental

F:107/Modified site: omega-N-methylarginine or omega-N-dimethylarginine (Arg) #

Query Match 100.0%; Score 94; DB 1; Length 171;  
Best Local Similarity 100.0%; Pred. No. 1.4e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVHFFKNIVTPRTP 17  
|||||

Db 83 ENPVHFFKNIVTPRTP 99

RESULT 5  
MBPG  
myelin basic protein - pig (tentative sequence)  
N:Alternate names: myelin A1 protein  
N:Contains: myelin basic protein amide 14  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 19-Apr-1996 #sequence \_revision 26-Apr-1996 #text\_change 09-Jul-2004  
C:Accession: A61640; A66245  
R:Kira, J.; Delbler, G.E.; Kruttsch, H.C.; Martenson, R.E.  
J. Neurochem. 44, 134-142, 1985  
A:Title: Amino acid sequence of porcine myelin basic protein.  
A:Reference number: A61640; MUID:85056964; PMID:2578056  
A:Accession: A61640  
A:Molecule type: protein  
A:Residues: 1-171 <KIR>  
A:Cross-references: UNIPROT:P81558  
A:Note: some peptides were ordered by homology  
R:Takamatsu, K.; Tatemoto, K.  
Biochem. Biophys. Res. Commun. 172, 1167-1174, 1990  
A:Title: Isolation and characterization of a novel peptide amide from porcine brain.  
A:Reference number: A36245; MUID:91058553; PMID:1700904  
A:Accession: A36245  
A:Molecule type: protein  
A:Residues: 1-14 <TK>  
A:Note: the sequence in the abstract is inconsistent with that in figure 3 in having Glu  
A:Note: this peptide has a carboxyl-terminal amide probably produced by a non-enzymatic  
C:Keywords: acetylated amino end; amidated carboxyl end; experimental autoimmune encephalomyelitis; myelin basic protein  
C:Keywords: acetylated amino end; amidated carboxyl end; experimental autoimmune encephalomyelitis; myelin basic protein  
F:1-171/Product: myelin basic protein #status experimental <MAY>  
F:1-14/Product: myelin peptide amide-14 #status experimental <PA12>  
F:14/Modified site: acetylated amino end (Ala) #status experimental  
F:14/Modified site: amidated carboxyl end (Tyr) (amide in mature form myelin peptide amide F:107/Modified site: omega-N-methylarginine or omega-N'-dimethylarginine (Arg))  
Query Match 100.0%; Score 94; DB 1; Length 171;  
Best Local Similarity 100.0%; Pred. No. 1.4e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVHFFNIVTPRP 17  
DB 83 ENPVHFFNIVTPRP 99

RESULT 6  
MBHUB  
myelin basic protein (validated) - human  
N:Contains: myelin basic protein precursor, 17.2K splice form; myelin basic protein precursor, 5K splice form  
C:Species: Homo sapiens (man)  
C:Date: 18-Dec-1981 #sequence\_revision 25-Aug-1995 #text\_change 09-Jul-2004  
C:Accession: S10483; A94106; B94106; A99256; JH0802; A60862; A61420; A33273; I54219; I56  
R:Streicher, R.; Scofield, W.  
Biochem. Biophys. Res. Commun. 370, 503-510, 1989  
A:Title: The organization of the human myelin protein gene. Comparison with the mouse myelin protein gene.  
A:Reference number: S10483; MUID:89302693; PMID:2472816  
A:Accession: S10482  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-197 <STR>  
A:Cross-references: UNIPROT:P02666; EMBL:X17286; NID:G34490; PIDN:CMA35179.1; PID:G11842  
R:Kamholz, J.; De Ferreira, P.; Puckett, C.; Lazzerini, R.  
Proc. Natl. Acad. Sci. U.S.A. 83, 4962-4966, 1986  
A:Title: Identification of three forms of human myelin basic protein by cDNA cloning.  
A:Reference number: A94106; MUID:86259714; PMID:2425357  
A:Accession: A94106  
A:Molecule type: mRNA  
A:Residues: 1-59, 86-197 <RAM>  
A:Cross-references: GB:M13577; NID:G187408; PIDN:AAA59562.1; PID:G307160  
A:Note: 18.5K splice form  
A:Accession: B94106  
A:Molecule type: mRNA  
A:Residues: 1-197 <KA2>

A:Note: antibody to the exon 2 encoded sequence detected a 21.5K splice form  
A:Note: a 17.2K splice form is also described  
A:Note: antibody to the exon 2 encoded sequence detected a 21.5K splice form; a 17.2K sp  
R:Carnegie, P.R.  
Biochem. J. 123, 57-67, 1971  
A:Title: Amino acid sequence of the encephalitogenic basic protein from human myelin.  
A:Reference number: A90256; MUID:72066400; PMID:4108501  
A:Accession: A90256  
A:Molecule type: protein  
A:Residues: 2-59, 86-197 <CAR>  
R:Probst, P.; Van Damme, J.; Opdenacker, G.  
Biochem. Biophys. Res. Commun. 192, 1175-1181, 1993  
A:Title: Leukocyte gelatinase B cleavage releases encephalitogens from human myelin basic  
A:Reference number: JH0802; MUID:93282820; PMID:7685161  
A:Accession: JH0802  
A:Molecule type: protein  
A:Residues: 2-59, 86-197 <PRO>  
A:Experimental source: brain  
R:Scoble, H.A.; Whitaker, J.N.; Biemann, K.  
J. Neurochem. 47, 614-616, 1986  
A:Title: Analysis of the primary sequence of human myelin basic protein peptides 1-44 and  
A:Reference number: A60862; MUID:86280476; PMID:2426402  
A:Accession: A60862  
A:Molecule type: protein  
A:Residues: 2-45, 117-197 <SCO>  
A:Note: evidence for acetylated amino end  
R:Gibson, B.W.; Gilliom, R.D.; Whitaker, J.N.; Biemann, K.  
J. Biol. Chem. 259, 5028-5031, 1984  
A:Title: Amino acid sequence of human myelin basic protein peptide 45-89 as determined by  
A:Reference number: A61420; MUID:84185608; PMID:6201481  
A:Accession: A61420  
A:Molecule type: protein  
A:Residues: 46-59, 86-116 <GIB>  
R:Wood, D.D.; Moscarello, M.A.  
J. Biol. Chem. 264, 5121-5127, 1989  
A:Title: The isolation, characterization, and lipid-aggregating properties of a citrullin  
A:Reference number: A33273; MUID:89174797; PMID:2466844  
A:Accession: A33273  
A:Molecule type: protein  
A:Residues: 15-25, 'X', 27-31, 'X', 33-59, 86-148, 'X', 150-156, 'X', 158-185, 'X', 187-196, 'X' <MOX>  
A:Note: form C-8; residues designated 'X' were determined as citrulline  
R:Balwin, G.S.; Carnegie, P.R.  
Biochem. J. 123, 69-74, 1971  
A:Title: Isolation and partial characterization of methylated arginines from the encephal  
A:Reference number: A90257; MUID:72066401; PMID:5128665  
A:Accession: A90257  
A:Contents: annotation: methylarginine  
A:Note: Arg-134 may be unmodified, monomethylarginine, or dimethylarginine in the approxi  
R:Lennon, V.A.; Wilks, A.V.; Carnegie, P.R.  
J. Immunol. 105, 1223-1230, 1970  
A:Reference number: A92806; MUID:71088405; PMID:4099924  
A:Accession: A92806  
A:Contents: annotation  
A:Note: a region including residues 139-149 induces experimental autoimmune encephalomyel  
R:Boylan, K.B.; Ayres, T.W.; Popko, B.; Takahashi, N.; Hood, L.E.; Prineas, S.B.  
Genomics 6, 16-22, 1990  
A:Title: Repetitive DNA (TGCA)n 5' to the human myelin basic protein gene: a new form of  
A:Reference number: I54219; MUID:90152679; PMID:1689270  
A:Accession: I54219  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-59 <RSC>  
A:Cross-references: GB:M63599; NID:G187402; PIDN:AAA59560.1; PID:G187403  
R:Noth, H.J.; Kronquist, K.E.; Kertler de Rosbo, N.; Crandall, B.F.; Campagnoni, A.T.  
J. Neurosci. Res. 17, 321-328, 1987  
A:Title: Evidence for the expression of four myelin basic protein variants in the develop  
A:Reference number: I56567; MUID:87711781; PMID:2442403  
A:Accession: I56567  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-132, 144-197 <RSC>  
A:Cross-references: GB:M30516; NID:G187410; PIDN:AAA59563.1; PID:G307161  
A:Accession: I73634  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA

A:Residues: 1-197 <RE3>  
A:Cross-references: GB:M30515; NID:G187412; PIDN:AAA59564.1; PID:G307162  
R:Roch, H.J.; Krontquist, K.; Precorius, P.J.; Crandall, B.F.; Campagnoni, A.T.  
J. Neurosci. Res. 16, 227-238, 1986  
A:Title: Isolation and characterization of a cDNA coding for a novel human 17.3K myelin  
A:Reference number: 156565; MUID:86308101; PMID:2427738  
A:Accession: 156565  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-59, 86-133, 145-197 <RE4>  
A:Cross-references: GB:M30047; NID:G187400; PIDN:AAA59559.1; PID:G307159  
R:Bouliaf, C.; Pang, H.; Mastroianni, F.; Moscarello, M.A.  
Arch. Biochem. Biophys. 332, 174-182, 1995  
A:Title: The isolation and characterization of four myelin basic proteins from the unbo  
A:Reference number: S66383; MUID:96004793; PMID:7574672  
A:Accession: S66383  
A:Molecule type: protein  
A:Residues: 23-25, 'X', 27-39 <BOU>  
A:Comment: Four alternatively spliced forms of myelin basic protein have been observed.  
C:Comment: Four alternatively spliced forms of myelin basic protein have been observed.  
C:Genetics:  
A:Gene: GDB:MBP  
A:Cross-references: GDB:119379; OMIM:159430  
A:Map position: 18q22-18qter  
A:Introns: 59/3; 85/3; 120/3; 132/3; 143/3; 183/3  
C:Function:  
A:Description: probably helps maintain myelin structure  
A:Superfamily: myelin basic protein  
C:Keywords: acetylated amino end; alternative splicing; citrulline; experimental autoimm  
F:2-197/Product: myelin basic protein, 21.5K splice form #status predicted <MAT1>  
F:2-132,144-197/Product: myelin basic protein, 20.2K splice form #status predicted <MAT2  
F:2-59,86-137/Product: myelin basic protein, 18.5K splice form #status predicted <MAT  
F:2-59,86-132,144-197/Product: myelin basic protein, 17.2K splice form #status predicted  
F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental  
F:26,32,149,187/Modified site: citrulline (Arg) (in form C-8) #status experimental  
F:134/Modified site: omega-N-methylarginine or omega-N, omega-N'-dimethylarginine (Arg) (

Query Match 100.0%; Score 94; DB 1; Length 197;  
Best Local Similarity 100.0%; Pred. No. 1.7e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRT 17  
110 ENPVVHFFKNIVTPRT 126  
Db

RESULT 7  
MEMSB  
goli1-myelin basic protein precursor - mouse  
N:Alternate names: goli1-mbp protein; MBP  
N:Contents: myelin basic protein  
C:Species: Mus musculus (house mouse)  
C:Dates: 17-Mar-1987 #sequence revision 07-Oct-1994 #ext change 09-Jul-2004  
A:Accession: A45421; B45421; A90867; A26591; A60920; 148407; 158996; 154  
R:Campagnoni, A.T.; Pribyl, T.M.; Campagnoni, C.W.; Kampf, K.; Amur-Umarjee, S.; Landry,  
J. Biol. Chem. 268, 4930-4938, 1993  
A:Title: Structure and developmental regulation of Goli1-mbp, a 105-kilobase gene that e  
A:Reference number: A45421; MUID:93186801; PMID:7680345  
A:Accession: A45421  
A:Molecule type: mRNA  
A:Residues: 1-190,217-276,316-328 <CAN1>  
A:Cross-references: UNIPROT:P04370; GB:L07507; NID:G193584  
A:Experimental source: clone J37  
A:Note: sequence extracted from NCBI backbone (NCBIN:126696) and modified  
A:Accession: B45421  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-191, 'SSEP' <CAN2>  
A:Cross-references: GB:L07508; NID:G193586; PIDN:AAA7721.1; PID:G193587  
A:Experimental source: clone BG21  
A:Note: sequence extracted from NCBI backbone (NCBIN:126700, NCBI:P126715)  
R:de Ferra, F.; Engh, H.; Hudson, L.; Kamholz, J.; Puckett, C.; Molineaux, S.; Lazzarini  
Cell 43, 721-727, 1985

A:Title: Alternative splicing accounts for the four forms of myelin basic protein.  
A:Reference number: A90875; MUID:86079555; PMID:2416470  
A:Accession: A90875  
A:Molecule type: mRNA  
A:Residues: 134-328 <DEF>  
A:Cross-references: GB:L00404; GB:M1669; NID:G199060; PIDN:AAA39502.1; PID:G387419  
R:Experimental source: 21.5K  
R:Takahashi, N.; Roach, A.; Tephlow, D.B.; Prusiner, S.B.; Hood, L.  
Cell 42, 139-148, 1985  
A:Title: Cloning and characterization of the myelin basic protein gene from mouse: one ge  
A:Reference number: A90867; MUID:85254913; PMID:2410136  
A:Accession: A90867  
A:Molecule type: DNA  
A:Residues: 134-190,217-328 <TAK>  
A:Cross-references: GB:M1533; NID:G199044; PIDN:AAA39496.1; PID:G387414  
A:Experimental source: 18.5K  
R:Newman, S.; Kitamura, K.; Campagnoni, A.T.  
Proc. Natl. Acad. Sci. U.S.A. 84, 886-890, 1987  
A:Title: Identification of a cDNA coding for a fifth form of myelin basic protein in mou  
A:Reference number: A94188; MUID:87118269; PMID:2433693  
A:Accession: A26591  
A:Molecule type: mRNA  
A:Residues: 134-274,316-328 <NEM1>  
A:Cross-references: GB:M15060; NID:G199048; PIDN:AA59711.1; PID:G199049  
A:Experimental source: clone M722; splice form 17.22K  
A:Accession: B26591  
A:Molecule type: mRNA  
A:Residues: 134-190,217-263,275-328 <NEM2>  
A:Cross-references: GB:M15063; NID:G199050  
A:Experimental source: clone M78; splice form 17.24K  
R:Kitamura, K.; Newman, S.L.; Campagnoni, C.W.; Verdi, J.M.; Mohandae, T.; Handley, V.W.;  
J. Neurochem. 54, 2032-2041, 1990  
A:Title: Expression of a novel transcript of the myelin basic protein gene.  
A:Reference number: A60920; MUID:90250449; PMID:1692584  
A:Accession: A60920  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 134-190,217-274,316-328 <KIT>  
A:Experimental source: M41; splice form 14K  
R:Grima, B.; Zelenika, D.; Pesac, B.  
J. Neurochem. 59, 2318-2323, 1992  
A:Title: A novel transcript overlapping the myelin basic protein gene.  
A:Reference number: 148407; MUID:93057537; PMID:1279125  
A:Accession: 148407  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-191, 'SSEP' <GRI>  
A:Cross-references: EMBL:X67319; NID:G51332; PIDN:CAA47733.1; PID:G51333  
A:Note: submitted to the EMBL Data Library, July 1992  
R:Zeller, N.K.; Hunkele, M.J.; Campagnoni, A.T.; Sprague, J.; Lazzarini, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 81, 18-22, 1984  
A:Title: Characterization of mouse myelin basic protein messenger RNAs with a myelin bas  
A:Reference number: 158996; MUID:84119431; PMID:1596644  
A:Accession: 158996  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 219-248 <ZEL>  
A:Cross-references: GB:K00989; NID:G199037; PIDN:AAA39495.1; PID:G54195  
R:Miura, M.; Tamura, T.  
Gene 75, 31-38, 1989  
A:Title: The promoter elements of the mouse myelin basic protein gene function efficient  
A:Reference number: 154033; MUID:89252919; PMID:2470651  
A:Accession: 154033  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 134-157 <MU>  
A:Cross-references: GB:M24410; NID:G199052; PIDN:AAA39498.1; PID:G554196  
R:Okano, H.; Tamura, T.; Miura, M.; Aoyama, A.; Ikenaka, K.; Oshimura, M.; Mikoshiba, K.  
EMBO J. 7, 77-83, 1988  
A:Title: Gene organization and transcription of duplicated MBP genes of myelin deficient  
A:Reference number: 153256; MUID:88196094; PMID:2452084  
A:Accession: 153256  
A:Status: translation not shown; translated from GB/EMBL/DBJ

A.Molecule type: DNA  
A.Residues: 217-229, 'NN', 232-250 <OKA>  
A.Cross-references: GB:M36275; NID:G159069; PIDN:AAA9504.1; PID:G293725  
A.Note: hypothetical translation of the reversed and complementary sequence to that shown  
C.Comment: Mice have five forms of myelin basic protein: 21.5K, 18.5K, 17.24K, 17.22K and  
C.Genetics:  
A.Gene: Goll1-mbp, shi-mld  
A.Introns: 190/3; 250/3; 262/3; 273/3; 314/3  
C.Function:  
A.Description: probably helps maintain myelin structure  
C.Superfamily: myelin basic protein  
C.Keywords: alternative splicing; myelin; structural protein  
F.1-190, 217-276, 316-328/Product: Goll1-mbp protein (clone J37) #status predicted <MA1>  
F.134-328/Product: myelin basic protein, splice form 21.5K #status predicted <MAT>  
F.134-274, 316-328/Product: myelin basic protein, splice form 17K-a #status predicted <MA1>  
F.134-190, 217-276, 316-328/Product: myelin basic protein, splice form 18.5K #status predicted <MA1>  
F.134-190, 217-276, 316-328/Product: myelin basic protein, splice form 17K-b #status predicted <MA1>  
F.134-190, 217-274, 316-328/Product: myelin basic protein, splice form 14K #status predicted <MA1>

Query Match 100.0%; Score 94; DB 1; Length 328;  
Best Local Similarity 100.0%; Pred. No. 3e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNITVPTPT 17  
DB 240 ENPVVHFFKNITVPTPT 256

RESULT 8  
S08535  
myelin basic protein - chicken  
C.Species: Gallus gallus (chicken)  
C.Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #ext\_change 09-Jul-2004  
C.Accession: S08535  
Gila 2, 241-249, 1989  
R.Zopf, D.; Somteag, V.; Betz, H.; Gundelfinger, E.D.  
A.Title: Developmental accumulation and heterogeneity of myelin basic protein transcript  
A.Reference number: S08535; MUID:89358239; PMID:2475444  
A.Accession: S08535  
A.Molecule type: mRNA  
A.Residues: 1-174 <ZOP>  
A.Cross-references: UNIPROT:P15720; EMBL:X17103; NID:G63594; PIDN:CAA4959.1; PID:G63595  
C.Superfamily: myelin basic protein

Query Match 92.6%; Score 87; DB 2; Length 174;  
Best Local Similarity 88.2%; Pred. No. 2.3e-07;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNITVPTPT 17  
DB 82 DNPVHFFKNITVPTPT 98

RESULT 9  
A60215  
myelin basic protein - dusky shark (fragments)  
C.Species: Carcharias obscurus (dusky shark)  
C.Date: 10-Nov-1992 #sequence\_revision 12-Mar-1993 #ext\_change 09-Jul-2004  
C.Accession: A60215  
J.Milne, T.J.; Atkins, A.R.; Warren, J.A.; Auton, W.P.; Smith, R.  
J. Neurochem. 55, 950-955, 1990  
A.Title: Shark myelin basic protein: amino acid sequence, secondary structure, and self-  
A.Reference number: A60215; MUID:90347482; PMID:1696624  
A.Accession: A60215  
A.Molecule type: protein  
A.Residues: 1-128 <MIL>  
A.Cross-references: UNIPROT:P98190  
A.Note: the source was designated as Carcharias obscurus (whaler shark)  
C.Superfamily: myelin basic protein

Query Match 63.8%; Score 60; DB 2; Length 128;  
Best Local Similarity 52.9%; Pred. No. 0.0065;  
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNITVPTPT 17  
DB 46 DSAVHFFKNMSPKAP 62

RESULT 10  
B32999  
myelin basic protein - horn shark  
C.Species: Heterodontus francisci (horn shark)  
C.Date: 21-Feb-1990 #sequence\_revision 21-Feb-1990 #ext\_change 09-Jul-2004  
C.Accession: B32999  
R.Saavedra, R.A.; Fors, L.; Aebersold, R.H.; Arden, B.; Horvath, S.; Sanders, J.; Hood, L.  
J. Mol. Evol. 29, 149-156, 1989  
A.Title: The myelin proteins of the shark brain are similar to the myelin proteins of the  
A.Reference number: A32999; MUID:90040744; PMID:2478717  
A.Accession: B32999  
A>Status: preliminary  
A.Molecule type: mRNA  
A.Residues: 1-155 <SAA>  
A.Cross-references: UNIPROT:P20939; GB:X17664; NID:G63974; PIDN:CAA35661.1; PID:G63975  
C.Superfamily: myelin basic protein

Query Match 56.4%; Score 53; DB 2; Length 155;  
Best Local Similarity 53.3%; Pred. No. 0.13;  
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNITVPTPT 15  
DB 72 DSAVHFFKNMSPK 86

RESULT 11  
G64440  
hypothetical protein MJ1128 - Methanococcus jannaschii  
C.Species: Methanococcus jannaschii  
C.Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #ext\_change 09-Jul-2004  
C.Accession: G64440  
R.Bull, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, J.; Reich, C.T.; Overbeek, R.; Kirschner, E.F.; Westbrook, K.G.; Merrick, J.M.; Glodok, A.; Ison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hult, M.A.  
Science 273, 1058-1073, 1996  
A.Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.  
A.Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.  
A.Reference number: A64300; MUID:96337999; PMID:8688087  
A.Accession: G64440  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A.Molecule type: DNA  
A.Residues: 1-308 <BUL>  
A.Cross-references: UNIPROT:Q58528; GB:U67555; GB:L77117; NID:G1591760; PIDN:AAB99130.1;  
C.Genetics:  
A.Map position: REV1069975-1069049  
A.Start codon: GTG  
C.Superfamily: hypothetical protein MJ1128

Query Match 47.9%; Score 45; DB 2; Length 308;  
Best Local Similarity 70.0%; Pred. No. 6.7;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ENPVVHFFKN 10  
DB 35 ENPVVHFFKN 44

RESULT 12  
A57246  
beta-lectorin precursor - chicken  
C.Species: Gallus gallus (chicken)  
C.Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #ext\_change 09-Jul-2004  
C.Accession: A57246  
R.Kilik, R.; Legan, P.K.; Malenczak, C.; Richardson, G.P.  
J. Cell Biol. 129, 535-547, 1995  
A.Title: Molecular cloning of chick beta-lectorin, an extracellular matrix molecule of ct

A:Reference number: A57246; MUID:95238547; PMID:7721949  
A:Accession: A57246  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-329 <KIL>  
C:Cross-references: UNIPROT:P54097; GB:L38519; NID:G602439; PIDN:AAA92461.1; PID:G602440  
C:Keywords: extracellular matrix; membrane protein; phosphatidylinositol linkage

Query Match 46.8%; Score 44; DB 2; Length 329;  
Best Local Similarity 53.8%; Pred. No. 11;  
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ENPVHFFKNIPT 13  
DB 91 KNPVHFFKNIPT 103

RESULT 13  
T46577  
Arylsulfatase (EC 3.1.6.1) [validated] - Neurospora crassa  
C:Species: Neurospora crassa  
C:Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 09-Jul-2004  
C:Accession: T46577  
R:Baker, D.L.; Paletta, J.V.  
A:Description: Molecular characterization of the arylsulfatase gene of Neurospora crassa  
A:Reference number: Z23090  
A:Accession: T46577  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-639 <BAK>  
A:Cross-references: UNIPROT:Q43113; EMBL:U89492; PIDN:AAC02716.1  
A:Experimental source: strain wild type 74-OR23-1A  
C:Genetics:  
A:Gene: ars-1  
A:Map position: 7  
A:Introns: 115/1; 518/3  
C:Function:  
A:Description: EC 3.1.6.1 [validated, MUID:89384589]  
A>Note: genes are expressed under conditions of sulfur limitation and are under coordinat  
C:Superfamily: plant sulfatase  
C:Keywords: sulfuric ester hydrolase

Query Match 46.8%; Score 44; DB 2; Length 639;  
Best Local Similarity 50.0%; Pred. No. 23;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 HFFKNIPTPT 17  
DB 282 HFFPVIVPTPT 293

RESULT 14  
S12904  
protein kinase (EC 2.7.1.37) - starfish (Pisaster ochraceus)  
C:Species: Pisaster ochraceus  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S12904  
R:Sanghera, J.S.; Aebersold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L.  
FEBS Lett. 273, 223-226, 1990  
A>Title: Identification of the sites in myelin basic protein that are phosphorylated by  
A:Reference number: S12904; MUID:91032186; PMID:1699809  
A:Accession: S12904  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <SAN>  
A:Cross-references: UNIPROT:Q7M3M4  
C:Keywords: phosphotransferase

Query Match 45.7%; Score 43; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.41;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NIVTPRTP 17  
DB 1 NIVTPRTP 8

RESULT 15  
C89965  
conserved hypothetical protein SA1613 [imported] - Staphylococcus aureus (strain N315)  
C:Species: Staphylococcus aureus  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: C89965  
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Imae, A.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratake, K.  
Lancet 357, 1225-1240, 2001  
A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
A:Reference number: A89758; MUID:21311952; PMID:11418146  
A:Accession: C89965  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-85 <KUR>  
A:Cross-references: UNIPROT:Q99775; GB:BA000018; PID:G13701588; PIDN:BA842881.1; GSPDB:G  
A:Experimental source: strain N315  
C:Genetics:  
A:Gene: SA1613  
C:Superfamily: conserved hypothetical protein H11000

Query Match 45.7%; Score 43; DB 2; Length 85;  
Best Local Similarity 35.7%; Pred. No. 3.3;  
Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 4 VHFKNIVTPRTP 17  
DB 8 MIFYQRFISPLTP 21

Search completed: June 7, 2005, 09:02:37  
Job time : 3.79102 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 08:39:41 ; Search time 8.36788 Seconds

(without alignments)  
1040.329 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94

Sequence: 1 ENPVVHFFKNIVTPRTP 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 segs, 512079187 residues 1612378

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : 1: uniprot\_sprot;\* 2: uniprot\_trembl;\* 3: uniprot\_swissprot;\* 4: uniprot\_gdb;\* 5: uniprot\_molmap;\* 6: uniprot\_ncbi;\* 7: uniprot\_pdb;\* 8: uniprot\_refseq;\* 9: uniprot\_trinity;\* 10: uniprot\_uniport;\* 11: uniprot\_uniport;\* 12: uniprot\_uniport;\* 13: uniprot\_uniport;\* 14: uniprot\_uniport;\* 15: uniprot\_uniport;\* 16: uniprot\_uniport;\* 17: uniprot\_uniport;\* 18: uniprot\_uniport;\* 19: uniprot\_uniport;\* 20: uniprot\_uniport;\* 21: uniprot\_uniport;\* 22: uniprot\_uniport;\* 23: uniprot\_uniport;\* 24: uniprot\_uniport;\* 25: uniprot\_uniport;\* 26: uniprot\_uniport;\* 27: uniprot\_uniport;\* 28: uniprot\_uniport;\* 29: uniprot\_uniport;\* 30: uniprot\_uniport;\* 31: uniprot\_uniport;\* 32: uniprot\_uniport;\* 33: uniprot\_uniport;\* 34: uniprot\_uniport;\* 35: uniprot\_uniport;\* 36: uniprot\_uniport;\* 37: uniprot\_uniport;\* 38: uniprot\_uniport;\* 39: uniprot\_uniport;\* 40: uniprot\_uniport;\* 41: uniprot\_uniport;\* 42: uniprot\_uniport;\* 43: uniprot\_uniport;\* 44: uniprot\_uniport;\* 45: uniprot\_uniport;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Score Match Length DB ID Description

1	94	100.0	74	2	Q6A164	Q6A164 homo sapien
2	94	100.0	158	2	Q8R4K6	Q8R4K6 rattus norv
3	94	100.0	160	2	Q6F104	Q6F104 homo sapien
4	94	100.0	167	1	MBP_CAVPO	P25188 cavia porce
5	94	100.0	168	1	MBP_RABIT	P25274 corycolagus
6	94	100.0	169	1	MBP_BOVIN	P02687 bos taurus
7	94	100.0	171	1	MBP_PANTR	P06906 pan troglod
8	94	100.0	171	1	MBP_PIG	P81588 sus scrofa
9	94	100.0	173	2	Q6J2R3	Q6J2R3 sus scrofa
10	94	100.0	180	2	Q6PK23	Q6PK23 homo sapien
11	94	100.0	194	1	MBP_RAT	P02688 rattus norv
12	94	100.0	203	2	Q6S2S4	Q6S2S4 homo sapien
13	94	100.0	250	1	MBP_MOUSE	P04370 mus musculu
14	94	100.0	304	1	MBP_HUMAN	P02686 homo sapien
15	87	92.6	173	1	MBP_CHICK	P15720 gallus galli
16	84	89.4	175	1	MBP_XENLA	P87346 xenopus lae
17	78	83.0	172	1	MBP_HORSE	P83487 equus caball
18	61	64.9	154	1	MBP_RAUER	Q91325 raja erinac
19	61	64.9	154	1	MBP_SQUAC	Q91439 squallus aca
20	60	63.8	128	2	P98190	P20999 heterodontu
21	53	56.4	154	1	MBP_HETFR	P20999 heterodontu
22	49.5	52.7	668	2	Q86T29	Q86T29 dictyosteli
23	47	50.0	300	2	Q86T29	Q86T29 dictyosteli
24	47	50.0	669	2	Q6DB87	Q6DB87 enterococcu
25	46	48.9	440	2	Q881D3	Q881D3 pseudomonas
26	46	48.9	440	2	Q881D3	Q881D3 pseudomonas
27	45	47.9	308	1	YB28_MENUA	YB28_MENUA xenopus lae
28	45	47.9	322	2	Q7VH19	Q7VH19 methanococc
29	45	47.9	441	2	Q965J5	Q965J5 helicobacte
30	45	47.9	759	2	Q8EE95	Q8EE95 caenorhabdi
31	44	46.8	215	2	Q7RJU7	Q7RJU7 plasmodium

32	44	46.8	329	1	TECB_CHICK	P54097 gallus galli
33	44	46.8	334	2	Q6N857	Q6N857 rhodospseudo
34	44	46.8	398	2	Q84H45	Q84H45 clostridium
35	44	46.8	501	2	Q7RJU8	Q7RJU8 plasmodium
36	44	46.8	527	2	Q6KHL8	Q6KHL8 mycoplasma
37	44	46.8	618	2	Q86ZNS	Q86ZNS podosporea a
38	44	46.8	639	2	Q43113	Q43113 neurospora
39	44	46.8	639	2	Q7RV09	Q7RV09 neurospora
40	43	45.7	14	2	Q7M3M4	Q7M3M4 pisaster oc
41	43	45.7	85	1	YG13_STRAN	P67305 staphylococ
42	43	45.7	85	1	YH33_STRAN	P67304 staphylococ
43	43	45.7	85	1	YH35_STRAN	P67304 staphylococ
44	43	45.7	85	1	Q6G8D8	Q6G8D8 staphylococ
45	43	45.7	85	2	Q6GFR2	Q6GFR2 staphylococ

## ALIGNMENTS

RESULT 1  
Q6A164 PRELIMINARY; PRT; 74 AA.  
ID Q6A164  
AC Q6A164  
DT 25-OCT-2004 (TREMBLrel). 28, Created  
DT 25-OCT-2004 (TREMBLrel). 28, Last sequence update  
DE 25-OCT-2004 (TREMBLrel). 28, Last annotation update  
DE Hypothetical protein DKFZp6810845 (Fragment).  
GN Name=DKFZp6810845;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Amygdala;  
RG The German CDNA Consortium;  
RA Othenmaelider B., Obermaier B., Deutschenbaur S., Schaalp A.,  
RA Mewes H.W., Weill B., Amlid C., Osanger A., Fobo G., Han M., Wiemann S.;  
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; CR627018; CAH10359.1; -;  
DR GO; GO:0019911; F:Structural constituent of myelin sheath; IEA.  
DR InterPro; IPR000548; Myelin\_BP.  
DR Pfam; PF01669; Myelin\_BP; 1.  
DR ProDom; PD004542; Myelin\_BP; 1.  
DR PROSITE; PS00569; MYELIN\_BP; 1.  
KW Hypothetical protein.  
FT NON\_TER 74  
SQ SEQUENCE 74 AA; 8265 MW; ACFE96ACBE9AE551 CRC64;  
Query Match 100.0%; Score 94; DB 2; Length 74;  
Best Local Similarity 100.0%; Pred. No. 5.8e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
Db 41 ENPVVHFFKNIVTPRTP 57  
RESULT 2  
Q8R4K6 PRELIMINARY; PRT; 158 AA.  
ID Q8R4K6  
AC Q8R4K6  
DT 01-JUN-2002 (TREMBLrel). 21, Created  
DT 01-JUN-2002 (TREMBLrel). 21, Last sequence update  
DT 01-MAR-2004 (TREMBLrel). 26, Last annotation update  
DE Myelin basic protein.  
GN Name=Mbp;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OC NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.

```

RC STRAIN=Sprague-Dawley;
RX MEDLINE=22941925; PubMed=14580679; DOI=10.1016/j.bbaexp.2003.08.010;
RA Matheue L., Blair G.E.;
RT "Identification and characterization of a cDNA encoding a 17-kDa
RN isoform of rat myelin basic protein.";
RM Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
RN NCBI_TaxId=10141;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Matheue L.M., Blair G.E.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF439750; AAL84189.1; -
DR GO; GO:0019911; F:structural constituent of myelin sheath; IEA.
DR InterPro; IPR000548; Myelin_BP.
DR Pfam; PF01669; Myelin_MBP; 1.
DR PRINTS; PR00212; MYELINMBP.
DR ProDom; PD004542; Myelin_BP; 1.
DR PROSITE; PS00569; MYELIN_MBP; 1.
SQ SEQUENCE 158 AA; 17240 MW; 3256580242EC3E1 CRC64;

Query Match 100.0%; Score 94; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
DB 81 ENPVVHFFKNIVTPRTP 97

RESULT 3
06FI04 PRELIMINARY; PRT; 160 AA.
AC 06FI04;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE MBP protein.

CN Name=MBP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neuber P., Ketrang K., Schalten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., Labaer J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR536534; CAG38771.1; -
DR GO; GO:0019911; F:structural constituent of myelin sheath; IEA.
DR InterPro; IPR000548; Myelin_BP.
DR Pfam; PF01669; Myelin_MBP; 1.
DR PRINTS; PR00212; MYELINMBP.
DR ProDom; PD004542; Myelin_BP; 1.
DR PROSITE; PS00569; MYELIN_MBP; 1.
SQ SEQUENCE 160 AA; 17347 MW; 0107AAD6053CD876 CRC64;

Query Match 100.0%; Score 94; DB 2; Length 160;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
DB 84 ENPVVHFFKNIVTPRTP 100

RESULT 4
MBP_CAVPO STANDARD; PRT; 167 AA.
AC P25188;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
FT

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DE Myelin basic protein (MBP).
CN Name=MBP;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
OX NCBI_TaxId=10141;
[1]
RP SEQUENCE.
RA MEDLINE=84215086; PubMed=6202840;
RA Delbier G.E., Martenson R.E., Krutzsch H.C., Kies M.W.;
RT "Sequence of guinea pig myelin basic protein.";
RL J. Neurochem. 43:100-105 (1984).
[2]
RP SEQUENCE OF 7-156 FROM N.A.
RC STRAIN=Hartley; TISSUE=Spinal cord;
RA Kim G., Tanuma N., Matsumoto Y.;
RT "DNA vaccination using Guinea pig myelin basic protein coding region
RN in experimental autoimmune encephalomyelitis.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE OF 45-87.
RA Shapira R., McKnearly S.S., Chou F., Kibler R.F.;
RT "Encephalitogenic fragment of myelin basic protein. Amino acid
RN sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";
RL J. Biol. Chem. 246:4630-4640 (1971).
[4]
RN POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=76025020; PubMed=51849;
RA Delbier G.E., Martenson R.E., Kramer A.J., Kies M.W.;
RT "The contribution of phosphorylation and loss of COOH-terminal
RN arginine to the microheterogeneity of myelin basic protein.";
RL J. Biol. Chem. 250:7931-7938 (1975).
CC -1- FUNCTION: Is, with PLP, the most abundant protein component of the
CC myelin membrane in the CNS. Has a role in both the formation and
CC stabilization of this compact multilayer arrangement of bilayers.
CC Each splice variant and charge isomer may have a specialized
CC function in the assembly of an optimized, biochemically functional
CC myelin membrane (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
CC -1- TISSUE SPECIFICITY: Found in both the central and the peripheral
CC nervous system.
CC -1- PTM: At least 5 charge isomers; C1 (the most cationic, least
CC modified, and most abundant form), C2, C3, C4 and C5 (the least
CC cationic form); are produced as a result of optional
CC posttranslational modifications such as phosphorylation of serine
CC or threonine residues, deamidation of glutamine or asparagine
CC residues, citrullination and methylation of arginine residues. C1
CC and C2 are unphosphorylated, C3 and C4 are monophosphorylated and
CC C5 is phosphorylated at two positions.
CC -1- SIMILARITY: Belongs to the myelin basic protein family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AF074337; AAC26130.1; -
DR F01; A37246; A37246.
DR HSSP; P02686; 1QCL.
DR InterPro; IPR000548; Myelin_BP.
DR Pfam; PF01669; Myelin_MBP; 1.
DR PRINTS; PR00212; MYELINMBP.
DR ProDom; PD004542; Myelin_BP; 1.
DR PROSITE; PS00569; MYELIN_MBP; 1.
DR Acetylation; Autoimmune encephalomyelitis; Citrullination;
DR Direct protein sequencing; Methylation; Myelin; Phosphorylation;
DR Structural protein.
FT DOMAIN 45 87 Induces experimental autoimmune
FT encephalomyelitis (EAE) 1.

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FT	DOMAIN	114	122		Induces experimental autoimmune encephalomyelitis (EAE) 2.
FT	MOD_RES	1	7		N-acetylalanine.
FT	MOD_RES	7	7		Phosphoserine (By similarity).
FT	MOD_RES	25	25		Citrulline (By similarity).
FT	MOD_RES	31	31		Citrulline (By similarity).
FT	MOD_RES	56	56		Phosphoserine (By similarity).
FT	MOD_RES	97	97		Phosphothreonine (By similarity).
FT	MOD_RES	102	102		Deamidated glutamine (partial) (By similarity).
FT	MOD_RES	106	106		Symmetric dimethylarginine (By similarity).
FT	MOD_RES	114	114		Phosphoserine (By similarity).
FT	MOD_RES	129	129		Citrulline (By similarity).
FT	MOD_RES	144	144		Deamidated glutamine (partial) (By similarity).
FT	MOD_RES	156	156		Citrulline (By similarity).
FT	MOD_RES	158	158		Phosphoserine (By similarity).
FT	MOD_RES	162	162		Phosphoserine (By similarity).
FT	MOD_RES	167	167		Citrulline (By similarity).
SO	SEQUENCE	167 AA;	18213 MW;		866D3JFISACEBA6 CRC64;
Query Match	Similarity	100.0%;	Score 94;	DB 1;	Length 167;
Best Local	Similarity	100.0%;	Pred. No. 1.3e-07;		
Matches	17;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
Qy	1 ENPVVHFFPKNIIVTRPT 17				
Db	82 ENPVVHFFPKNIIVTRPT 98				
RESULT 5					
MBP_RABIT	ID_MBP_RABIT	STANDARD;	PRT;	168 AA.	
AC	P25274;				
DT	01-MAY-1992 (Rel. 22, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	05-JUL-2004 (Rel. 44, Last annotation update)				
DE	Myelin basic protein (MBP) (Myelin P1 protein).				
GN	Name=MBP;				
OS	Oryctolagus cuniculus (Rabbit).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.				
OX	NCBI_TaxId=9986;				
RN	[1]				
RP	PRELIMINARY SEQUENCE.				
RC	TISSUE=Sciatic nerve;				
RX	MEDLINE=73190037; PubMed=4662101;				
RA	Brostoff S.W., Bylar E.H.;				
RT	"The proposed amino acid sequence of the P1 protein of rabbit sciatic nerve myelin.";				
RL	Arch. Biochem. Biophys. 153:590-598(1972).				
RN	[2]				
RP	SEQUENCE OF 45-86.				
RA	Shapiro R., McKeally S.S., Chou F., Kihler R.F.;				
RT	"Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";				
RL	J. Biol. Chem. 246:4630-4640(1971).				
RN	[3]				
RP	PHOSPHORYLATION.				
RX	MEDLINE=83108902; PubMed=6185481;				
RA	Martenson R.E., Law M.O., Deliber G.B.;				
RT	"Identification of multiple in vivo phosphorylation sites in rabbit myelin basic protein.";				
RL	J. Biol. Chem. 258:930-937(1983).				
CC	-I- FUNCTION: Is, with PLP, the most abundant protein component of the myelin membrane in the CNS. Has a role in both the formation and stabilization of this compact multilayer arrangement of bilayers. Each splice variant and charge isoform may have a specialized function in the assembly of an optimized, biochemically functional myelin membrane (By similarity).				
CC	-I- SUBUNIT: Homodimer (By similarity).				
CC	-I- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.				

CC	-1- TISSUE SPECIFICITY:	Found in both the central and the peripheral nervous system.
CC	-1- PTM:	As in other animals, several charge isoforms may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.
CC	-1- PTM:	The N-terminus is blocked.
CC	-1- SIMILARITY:	Belongs to the myelin basic protein family.
DR	HSPB; P02686;	10CLL.
DR	InterPro;	IPIR000548; Myelin BP.
DR	Pfam;	PF01669; Myelin_MBP_1.
DR	PRINTS;	PR00212; MYELINMBP.
DR	PRODOM;	PD004542; Myelin_BP_1.
DR	PROSITE;	PS00569; MYELIN_MB_P1.
KW	Acetylation;	Autoimmune encephalomyelitis; Citrullination;
RK	Direct protein sequencing;	Methylation; Myelin; Phosphorylation;
KM	Structural Protein.	
FT	DOMAIN	45      86      Induces experimental autoimmune encephalomyelitis (EAE).
FT	MOD_RES	1      7      N-acetylalanine (probable).
FT	MOD_RES	7      7      Phososerine.
FT	MOD_RES	25    25    Citrulline (By similarity).
FT	MOD_RES	31    31    Citrulline (By similarity).
FT	MOD_RES	56    56    Phososerine.
FT	MOD_RES	96    96    Phosphothreonine.
FT	MOD_RES	101   101   Deamidated glutamine (partial) (Probable).
FT	MOD_RES	105   105   Omega-N-methylarginine (partial).
FT	MOD_RES	105   105   Symmetric dimethylarginine (partial).
FT	MOD_RES	113   113   Phososerine.
FT	MOD_RES	128   128   Citrulline (By similarity).
FT	MOD_RES	145   145   Deamidated glutamine (partial) (By similarity).
FT	MOD_RES	157   157   Citrulline (By similarity).
FT	MOD_RES	159   159   Phososerine (By similarity).
FT	MOD_RES	163   163   Phososerine.
FT	MOD_RES	168   168   Citrulline (By similarity).
FT	CONFLICT	46    46    S -> G (in Ref. 2).
SQ	SEQUENCE	168 AA; 18217 MW; EC3C97ACD2C08EA6 CRC64;
Oy	Query Match	Score 94; DB 1; Length 168; Best Local Similarity 100.0%; Pred. No. 1.3e-07; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Dd	Db	1 ENPVVHFKNIVTPRT 17           81 ENPVVHFKNIVTPRT 97
<hr/>		
RESULT 6	ID MBP_BOVIN STANDARD; PTR; 169 AA.	
OC POZ687; O9BCG8; Q9TSA6; Q9TSA6;		
DT 21-JUL-1986 (Rel. 01, Created)		
DT 21-JUL-1986 (Rel. 01, Last sequence update)		
DT 05-JUN-2004 (Rel. 44, Last annotation update)		
DE Myelin basic protein (MBP) (Myelin AI protein) (20 kDa microtubule stabilizing protein).		
CN Name-MBP:		
OS Bos taurus (Bovine).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC Bovinae; Bos.		
NCBI_TaxID=9913;		
[1]		
RP SEQUENCE		
RX MEDLINE=72007306; PubMed=5096093;		
RA Eyler A.H., Brostoff S.W., Hashim G., Caccam J., Burnett P.;		
RT "Basic Al protein of the myelin membrane. The complete amino acid sequence.";		
J. Biol. Chem. 246:5770-5784(1971).		
[2]		

RP REVISION.  
RX MEDLINE=74070688; PubMed=4129204;  
RA Brostoff S.W., Reuter W., Hichens M., Eylar E.H.;  
RT "Specific cleavage of the A1 protein from myelin with cathepsin D.";  
RL J. Biol. Chem. 249:559-567(1974).  
[3]  
RP SEQUENCE OF 4-56 FROM N.A.  
RA Piotrowski D., Medugorac I., Foerster M.;  
RT "A new MBP allele in Bos taurus is characterized by BseI PCR-RFLP";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
[4]  
RP SEQUENCE OF 43-87.  
RA Shapira R., McKneally S.S., Chou F.C.-H., Kibler R.F.;  
RT "Encephalogenic fragment of myelin basic protein. Amino acid  
sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";  
RL J. Biol. Chem. 246:4630-4640(1971).  
[5]  
RP SEQUENCE OF 38-58 AND 119-141.  
RA TISSUE=Brain;  
RX MEDLINE=93003019; PubMed=1382581;  
RA Pirotte F., Derancourt J., Hache J., Job D., Margolis R.L.;  
RT "Ca(2+)-calmodulin regulated effectors of microtubule stability in  
bovine brain.";  
RL Biochemistry 31:8849-8855(1992).  
[6]  
RP SEQUENCE OF 30-42; 74-89 AND 114-129.  
RX MEDLINE=96107211; PubMed=8530487; DOI=10.1074/jbc.270.51.30551;  
RA Praad K., Barouch W., Martin B.M., Greene L.E., Eisenberg E.;  
RT "Purification of a new clathrin assembly protein from bovine brain  
coated vesicles and its identification as myelin basic protein.";  
RL J. Biol. Chem. 270:30551-30556(1995).  
[7]  
RP SYNTHESIS OF ALLERGIC ENCEPHALOMYELITIS INDUCING REGION.  
RX MEDLINE=70178977; PubMed=5442707;  
RA Eylar E.H., Caccam J., Jackson J.J., Westall F.C., Robinson A.B.;  
RT "Experimental allergic encephalomyelitis: synthesis of disease-  
inducing site of the basic protein.";  
RL Science 168:1220-1223(1970).  
[8]  
RP METHYLATION.  
RX MEDLINE=71153946; PubMed=4994464;  
RA Brostoff S.W., Eylar E.H.;  
RT "Localization of methylated arginine in the A1 protein from myelin.";  
RL Proc. Natl. Acad. Sci. U.S.A. 68:765-769(1971).  
[9]  
RP POST-TRANSLATIONAL MODIFICATIONS.  
RX MEDLINE=76167591; PubMed=57115;  
RA Chou F.C.-H., Chou C.-H.J., Shapira R., Kibler R.F.;  
RT "Basis of microheterogeneity of myelin basic protein.";  
RL J. Biol. Chem. 251:2671-2679(1976).  
[10]  
RP SEQUENCE OF 97-104, AND PHOSPHORYLATION SITE THR-97.  
RX MEDLINE=91060584; PubMed=1700979;  
RA Erickson A.K., Payne D.M., Martino P.A., Rosomando A.J.,  
RA Shabanowitz J., Weber M.J., Hunt D.F., Sturgill T.W.;  
RT "Identification by mass spectrometry of threonine 97 in bovine myelin  
basic protein as a specific phosphorylation site for mitogen-activated  
protein kinase.";  
RL J. Biol. Chem. 265:19728-19735(1990).  
[11]  
RP POST-TRANSLATIONAL MODIFICATIONS.  
RX MEDLINE=98153125; PubMed=9485392; DOI=10.1021/bj972347c;  
RA Zand R., Li M.X., Jin X., Lubman D.;  
RT "Determination of the sites of posttranslational modifications in the  
chargin isomers of bovine myelin basic protein by capillary  
electrophoresis-mass spectroscopy.";  
RL Biochemistry 37:2441-2448(1998).  
[12]  
RP DIMERIZATION.  
RX MEDLINE=80198320; PubMed=6155143;  
RA Smith R.;  
RT "Sedimentation analysis of the self-association of bovine myelin basic  
protein.";

RL Biochemistry 19:1826-1831(1980).  
CC -1- FUNCTION: Is, with PLP, the most abundant protein component of the  
CC myelin membrane in the CNS. Has a role in both the formation and  
CC stabilization of this compact multilayer arrangement of bilayers.  
CC Each splice variant and charge isomer may have a specialized  
CC function in the assembly of an optimized, biochemically functional  
CC myelin membrane (By similarity).  
CC -1- SUBUNIT: Homodimer; self-associates in the presence of lysolipid.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.  
CC -1- TISSUE SPECIFICITY: Found in both the central and the peripheral  
CC nervous system.  
CC -1- PTM: At least 6 charge isomers; C1 (the most cationic and least  
CC modified form), C2, C3, C4, C5 and C6 (the least cationic form);  
CC are produced as a result of optional posttranslational  
CC modifications, such as phosphorylation of serine or threonine  
CC residues, deamidation of glutamine or asparagine residues,  
CC citrullination and methylation of arginine residues.  
CC -1- SIMILARITY: Belongs to the myelin basic protein family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
CC EMBL; AF226693; AAK0645.1; -.  
CC PIR; A92089; MBOB.  
CC HSSP; P02686; 10CL.  
CC InterPro: IPR000548; Myelin BP.  
CC Pfam; PF01669; Myelin MBP; 1.  
CC PRINTS; PR00212; MYELINBP.  
CC ProDom; PD004542; Myelin BP; 1.  
CC PROSITE; PS00569; MYELIN MBP; 1.  
KW Acetylcholine; Autoimmune encephalomyelitis; Citrullination;  
KW Direct protein sequencing; Methylation; Myelin; Phosphorylation;  
KW Structural protein.  
FT DOMAIN 43 87  
FT Induces experimental autoimmune  
FT encephalomyelitis (EAE) 1.  
FT Induces experimental autoimmune  
FT encephalomyelitis (EAE) 2.  
FT N-acetylgalanine.  
FT Phosphoserine (in C5 and C6).  
FT Citrulline (By similarity).  
FT Citrulline (By similarity).  
FT Phosphoserine (in C4, C5 and C6).  
FT Phosphoserine (in C4, C5 and C6).  
FT Phosphoserine (in C4, C5 and C6).  
FT Citrulline (Probable).  
SQ SEQUENCE 169 AA; 18323 MW; 8E1157B7A1978484 CRC64;  
Query Match 100.0%; Score 94; DB 1; Length 169;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
Db 82 ENPVVHFFKNIVTPRTP 98  
RESULT 7  
MBP\_PANTR  
ID\_MBP\_PANTR STANDARD; PRT; 171 AA.

AC P06906; 01-JAN-1988 (rel. 06, Created)  
DT 01-JAN-1988 (rel. 06, Last sequence update)  
DT 25-OCT-2004 (rel. 45, Last annotation update)  
DE Myelin basic protein (MBP).  
GN Name=MBP;  
OS Pan troglodytes (chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
OX NCBI\_TaxID=9598;  
RN [1]  
RP PRELIMINARY SEQUENCE.  
RX MEDLINE=76009821; PubMed=51459; DOI=10.1016/0024-3205(75)90506-8;  
RT Westall F.C., Thompson W., Katter S.S.;  
RT "The proposed sequence of the encephalitogenic protein from chimpanzee brain."  
RL Life Sci. 17:219-223(1975).  
CC -1- FUNCTION: Is, with PLP, the most abundant protein component of the myelin membrane in the CNS. Has a role in both the formation and stabilization of this compact multilayer arrangement of bilayers. Each splice variant and charge isomer may have a specialized function in the assembly of an optimized, biochemically functional myelin membrane (By similarity).  
CC -1- SUBUNIT: Homodimer (By similarity).  
CC -1- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.  
CC -1- SIMILARITY: Belongs to the myelin basic protein family.  
DR PIR: A01139; MRCZB.  
DR HSSP: P02686; IQCL.  
DR InterPro: IPR000548; Myelin\_BP.  
DR Pfam: PF01659; Myelin\_MBP; I.  
DR PRINTS: PR00212; MYELINBP.  
DR ProDom: PD004542; Myelin\_BP; 1.  
DR PROSITE: PS00569; MYELIN\_MBP; 1.  
KW Acetylation; Autoimmune encephalomyelitis; Citrullination; Direct protein sequencing; Methylation; Myelin; Phosphorylation; Structural protein.  
FT MOD\_RES 1 1 N-acetylation.  
FT MOD\_RES 7 7 Phosphoserine (By similarity).  
FT MOD\_RES 25 25 Citrulline (By similarity).  
FT MOD\_RES 31 31 Citrulline (By similarity).  
FT MOD\_RES 56 56 Phosphoserine (By similarity).  
FT MOD\_RES 98 98 Phosphothreonine (By similarity).  
FT MOD\_RES 103 103 Deamidated glutamine (partial) (By similarity).  
FT MOD\_RES 107 107 Omega-N-methylated arginine.  
FT MOD\_RES 115 115 Phosphoserine (By similarity).  
FT MOD\_RES 122 122 Citrulline (By similarity).  
FT MOD\_RES 130 130 Citrulline (By similarity).  
FT MOD\_RES 148 148 Deamidated glutamine (partial) (By similarity).  
FT MOD\_RES 160 160 Citrulline (By similarity).  
FT MOD\_RES 162 162 Phosphoserine (By similarity).  
FT MOD\_RES 166 166 Phosphoserine (By similarity).  
FT MOD\_RES 171 171 Citrulline (By similarity).  
SQ SEQUENCE 171 AA; 18560 MW; E9FED59DE633293 CRC64;  
Query Match 100.0%; Score 94; DB 1; Length 171;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Mismatches 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
DB 83 ENPVVHFFKNIVTPRTP 99  
RESULT 8  
MBP\_PIG STANDARD; PRT; 171 AA.  
ID\_MBP\_PIG

AC P01558; P98189; 30-MAY-2000 (rel. 39, Created)  
DT 30-MAY-2000 (rel. 39, Last sequence update)  
DT 05-JUL-2004 (rel. 44, Last annotation update)  
DE Myelin basic protein (MBP).  
GN Name=MBP;  
OS Sus scrofa (pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE, AND METHYLATION OF ARG-107.  
RX TISSUE=Brain;  
RX MEDLINE=85056964; PubMed=2578056;  
RT Kira J.-I., Delbier G.E., Krutzsch H.C., Martenson R.E.;  
RT "Amino acid sequence of porcine myelin basic protein."  
RL J. Neurochem. 44:134-142(1985).  
RN [2]  
RP ERRATUM.  
RA Kira J.-I., Delbier G.E., Krutzsch H.C., Martenson R.E.;  
RL J. Neurochem. 44:1663-1663(1985).  
CC -1- FUNCTION: Is, with PLP, the most abundant protein component of the myelin membrane in the CNS. Has a role in both the formation and stabilization of this compact multilayer arrangement of bilayers. Each splice variant and charge isomer may have a specialized function in the assembly of an optimized, biochemically functional myelin membrane (By similarity).  
CC -1- SUBUNIT: Homodimer (By similarity).  
CC -1- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.  
CC -1- SIMILARITY: Belongs to the myelin basic protein family.  
DR PIR: A61640; MBPG.  
DR HSSP: P02686; IQCL.  
DR InterPro: IPR000548; Myelin\_BP.  
DR Pfam: PF01659; Myelin\_MBP; I.  
DR PRINTS: PR00212; MYELINBP.  
DR ProDom: PD004542; Myelin\_BP; 1.  
DR PROSITE: PS00569; MYELIN\_MBP; 1.  
KW Acetylation; Citrullination; Direct protein sequencing; Methylation; Myelin; Phosphorylation; Structural protein.  
FT MOD\_RES 1 1 N-acetylation.  
FT MOD\_RES 7 7 Phosphoserine (By similarity).  
FT MOD\_RES 25 25 Citrulline (By similarity).  
FT MOD\_RES 31 31 Citrulline (By similarity).  
FT MOD\_RES 55 55 Phosphoserine (By similarity).  
FT MOD\_RES 98 98 Phosphothreonine (By similarity).  
FT MOD\_RES 103 103 Deamidated glutamine (partial) (By similarity).  
FT MOD\_RES 107 107 Omega-N-methylated arginine (partial).  
FT MOD\_RES 107 107 Symmetric dimethylarginine (partial).  
FT MOD\_RES 115 115 Phosphoserine (By similarity).  
FT MOD\_RES 130 130 Citrulline (By similarity).  
FT MOD\_RES 148 148 Deamidated glutamine (partial) (By similarity).  
FT MOD\_RES 160 160 Citrulline (By similarity).  
FT MOD\_RES 162 162 Phosphoserine (By similarity).  
FT MOD\_RES 166 166 Phosphoserine (By similarity).  
FT MOD\_RES 171 171 Citrulline (By similarity).  
SQ SEQUENCE 171 AA; 18487 MW; 287MEDP2F2402BD9 CRC64;  
Query Match 100.0%; Score 94; DB 1; Length 171;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Mismatches 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
DB 83 ENPVVHFFKNIVTPRTP 99

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RESULT 9
ID 0612R3 PRELIMINARY; PRT; 173 AA.
AC 0602R3;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE Myelin basic protein.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OC NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim J.G., Noneman D., Vallet J.L., Rohrer G.A., Christenson R.K.;
RA Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY603684; AAT28338.1;
DR GO; GO:0019911; F:Structural constituent of myelin sheath; IEA.
DR InterPro; IPR000548; Myelin_BP.
DR Pfam; PF01669; Myelin_MBP; I.
DR PRINTS; PR00212; MYELINMBP.
DR PRODOM; PD004542; Myelin_BP; 1.
DR PROSITE; PS00569; MYELIN_MBP; 1.
SQ SEQUENCE 173 AA; 18731 MW; 6684D01E66081AA CRC64;

Query Match 100.0%; Score 94; DB 2; Length 173;
Best Local Similarity 100.0%; Fred. No. 1.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVFFKNIVTPRT 17
DB 65 ENPVVFFKNIVTPRT 101
RESULT 10
ID 06PK23 PRELIMINARY; PRT; 180 AA.
AC 06PK23;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE MBP protein (Fragment).
GN Name=MBP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Skin.
RA MEDLINE=23289257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strussberg R.;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schaller G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares W.B., Donald D., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ushin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Skalko U., Smalins D.E., Scherch A., Schein J.E.,
RA Krzywinski M.I., Skalko U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences.";
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP SEQUENCE FROM N.A.

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RC TISSUE=Skin;
RA Strussberg R.;
RA Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC008749; AA08749.2;
DR GO; GO:0019911; F:Structural constituent of myelin sheath; IEA.
DR InterPro; IPR000548; Myelin_BP.
DR Pfam; PF01669; Myelin_MBP; I.
DR PRINTS; PR00212; MYELINMBP.
DR PRODOM; PD004542; Myelin_BP; 1.
DR PROSITE; PS00569; MYELIN_MBP; 1.
FT NON TER 1
SQ SEQUENCE 180 AA; 19465 MW; D9EA204F92BD7024 CRC64;

Query Match 100.0%; Score 94; DB 2; Length 180;
Best Local Similarity 100.0%; Fred. No. 1.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVFFKNIVTPRT 17
DB 93 ENPVVFFKNIVTPRT 109
RESULT 11
ID MBP_RAT STANDARD; PRT; 194 AA.
AC P02688; Q921J4; Q921J6;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Myelin basic protein s (MBP S).
GN Name=MBP;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
RA Lobell A.M., Wiggall H.;
RA Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RA MEDLINE=87026249; PubMed=2429678;
RA Schach M., Budzinski R.M., Stofel W.;
RA "Cloned proteolipid protein and myelin basic protein cDNA.
RA Transcription of the two genes during myelination.";
RA Biol. Chem. Hoppe-Seyler 367:825-834(1986).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RA MEDLINE=84026484; PubMed=6194889; DOI=10.1016/0092-8674(83)90536-6;
RA Roach A., Boylan K.B., Horvath S., Prusiner S.B., Hood L.E.;
RA "Characterization of cloned cDNA representing rat myelin basic
RA protein: absence of expression in brain of shiverer mutant mice.";
RA Cell 34:799-806(1983).
RN [4]
RP SEQUENCE (ISOFORM 4).
RA MEDLINE=75127359; PubMed=411893;
RA Dunkley P.R., Carnegie P.R.;
RA "Amino acid sequence of the smaller basic protein from rat brain
RA myelin.";
RA Biochem. J. 141:243-255(1974).
RN [5]
RP SEQUENCE OF 130-194 FROM N.A.
RA STRAIN=Lewis; TISSUE=Brain;
RA MEDLINE=96078224; PubMed=7578863;
RA Malocka J., Dormair K.;
RA "Alternative splicing and cDNA sequence of myelin basic protein gene
RA of the Lewis rat.";
RA Autoimmunity 20:67-68(1995).
RN [6]
RP SEQUENCE OF 45-111 (ISOFORM 4).
RA MEDLINE=73180720; PubMed=4122324;
RA McFarlin D.E., Blank S.E., Kibler R.F., McKeally S.S., Shapiro R.;
RA "Experimental allergic encephalomyelitis in the rat: response to

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OM protein - protein search, using sw model

Run on: June 7, 2005, 09:01:44 ; Search time 7.45769 Seconds  
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Title: US-10-000-439-13

Perfect score: 94  
Sequence: 1 ENPVVHFFKNIVTPRTP 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1599520 seqs, 360203123 residues

Total number of hits satisfying chosen parameters: 1599520

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA.\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
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5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
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20: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
21: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	100.0	17	US-10-104-973-3	Sequence 3, Appl1
2	94	100.0	17	US-10-000-439-13	Sequence 13, Appl1
3	94	100.0	17	US-10-362-264-1	Sequence 1, Appl1
4	94	100.0	17	US-10-233-892A-2	Sequence 2, Appl1
5	94	100.0	17	US-10-482-044-5	Sequence 5, Appl1
6	94	100.0	19	US-09-740-003-2	Sequence 1, Appl1
7	94	100.0	19	US-09-768-872-1	Sequence 1, Appl1
8	94	100.0	19	US-09-766-378A-32	Sequence 32, Appl1
9	94	100.0	19	US-10-239-313A-143	Sequence 143, Appl1
10	94	100.0	19	US-10-743-398-2	Sequence 2, Appl1
11	94	100.0	20	US-09-766-378A-28	Sequence 28, Appl1
12	94	100.0	20	US-09-836-433-30	Sequence 30, Appl1

13	94	100.0	20	11	US-09-859-012-35	Sequence 35, Appl1
14	94	100.0	20	11	US-09-859-012-49	Sequence 49, Appl1
15	94	100.0	21	13	US-10-081-281-33	Sequence 33, Appl1
16	94	100.0	23	9	US-09-909-460-1	Sequence 1, Appl1
17	94	100.0	23	11	US-09-872-886-1	Sequence 1, Appl1
18	94	100.0	24	15	US-10-149-138-4219	Sequence 4219, Ap
19	94	100.0	24	15	US-10-149-135-2206	Sequence 2206, Ap
20	94	100.0	24	16	US-10-149-138-4219	Sequence 4219, Ap
21	94	100.0	46	9	US-09-813-383-1	Sequence 1, Appl1
22	94	100.0	46	9	US-09-813-463A-1	Sequence 1, Appl1
23	94	100.0	46	11	US-09-813-463A-1	Sequence 1, Appl1
24	94	100.0	157	16	US-10-425-115-339675	Sequence 339675, Appl1
25	94	100.0	169	16	US-10-475-104-32	Sequence 32, Appl1
26	94	100.0	170	13	US-10-015-540-2	Sequence 2, Appl1
27	94	100.0	170	14	US-10-199-995-3	Sequence 3, Appl1
28	94	100.0	171	8	US-08-484-409-2	Sequence 2, Appl1
29	94	100.0	171	9	US-09-989-476-2	Sequence 2, Appl1
30	94	100.0	171	9	US-09-947-770-4	Sequence 4, Appl1
31	94	100.0	171	9	US-09-893-348-12	Sequence 12, Appl1
32	94	100.0	171	10	US-09-218-277-12	Sequence 12, Appl1
33	94	100.0	171	13	US-10-104-973-2	Sequence 2, Appl1
34	94	100.0	171	14	US-10-000-439-12	Sequence 12, Appl1
35	94	100.0	171	14	US-10-270-707-2	Sequence 2, Appl1
36	94	100.0	171	16	US-10-772-656-102	Sequence 102, Appl1
37	94	100.0	171	16	US-10-466-220A-1	Sequence 1, Appl1
38	94	100.0	171	16	US-10-820-983-2	Sequence 2, Appl1
39	94	100.0	171	16	US-10-810-653-12	Sequence 12, Appl1
40	94	100.0	180	16	US-10-425-115-339677	Sequence 339677, Appl1
41	94	100.0	189	13	US-10-087-192-1470	Sequence 1470, Ap
42	94	100.0	197	14	US-10-270-877-54	Sequence 54, Appl1
43	94	100.0	197	14	US-10-270-837-54	Sequence 54, Appl1
44	94	100.0	197	16	US-10-772-656-53	Sequence 53, Appl1
45	94	100.0	207	13	US-10-081-281-93	Sequence 93, Appl1

#### ALIGNMENTS

RESULT 1  
US-10-104-973-3  
; Sequence 3, Application US/10104973  
; Publication No. US20020176866A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaur, Amitabh  
; APPLICANT: Conlon, Paul J.  
; APPLICANT: Ling, Nicholas C.  
; APPLICANT: Staehlin, Theophil  
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING  
; TITLE OF INVENTION: PEPTIDE ANALOGS OF HUMAN MYELIN BASIC PROTEIN  
; FILE REFERENCE: 690068.405C4  
; CURRENT APPLICATION NUMBER: US/10/104,973  
; CURRENT FILING DATE: 2002-03-20  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase  
US-10-104-973-3

Query Match 100.0%; Score 94; DB 13; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.6e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
Db 1 ENPVVHFFKNIVTPRTP 17

RESULT 2  
US-10-000-439-13  
; Sequence 13, Application US/10000439  
; Publication No. US20030064063A1  
; GENERAL INFORMATION:  
; APPLICANT: Saxon, Andrew  
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR  
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES  
; FILE REFERENCE: UC067.004A  
; CURRENT APPLICATION NUMBER: US/10/000,439  
; PRIOR FILING DATE: 2001-10-24  
; PRIOR APPLICATION NUMBER: US 09/847,208  
; PRIOR FILING DATE: 2001-05-01  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO: 13  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-000-439-13

Query Match 100.0%; Score 94; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.6e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
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DB 1 ENPVVHFFKNIVTPRTP 17

RESULT 3  
US-10-362-264-1  
; Sequence 1, Application US/10362264  
; Publication No. US20030191063A1  
; GENERAL INFORMATION:  
; APPLICANT: Wraith, David  
; APPLICANT: Anderson, Stephen  
; APPLICANT: Mazza, Graziella  
; APPLICANT: Ponsford, Mary  
; APPLICANT: Streeter, Heather  
; APPLICANT: The University of Bristol  
; TITLE OF INVENTION: PEPTIDE SELECTION METHOD  
; FILE REFERENCE: 1433.004US1  
; CURRENT APPLICATION NUMBER: US/10/362,264  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: PCT/GB01/03702  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 0020618.5  
; PRIOR FILING DATE: 2000-08-21  
; PRIOR APPLICATION NUMBER: 0114547.3  
; PRIOR FILING DATE: 2001-06-14  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 1  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-362-264-1

Query Match 100.0%; Score 94; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.6e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ENPVVHFFKNIVTPRTP 17

RESULT 4  
US-10-233-892A-2  
; Sequence 2, Application US/10233892A  
; Publication No. US20040043431A1  
; GENERAL INFORMATION:

; APPLICANT: Vojdani, Aristo  
; TITLE OF INVENTION: DIAGNOSIS OF MULTIPLE SCLEROSIS AND  
; TITLE OF INVENTION: OTHER DEMENTIATING DISEASES  
; FILE REFERENCE: IMSMS.001A  
; CURRENT APPLICATION NUMBER: US/10/233,892A  
; CURRENT FILING DATE: 2002-08-29  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO: 2  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Human Myelin Binding Protein Sequence 83-89  
US-10-233-892A-2

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Best Local Similarity 100.0%; Pred. No. 4.6e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ENPVVHFFKNIVTPRTP 17

RESULT 5  
US-10-482-044-5  
; Sequence 5, Application US/10482044  
; Publication No. US20040235713A1  
; GENERAL INFORMATION:  
; APPLICANT: Anna Maria PAPINI et al  
; TITLE OF INVENTION: Glycopeptides, their preparation and use in the diagnosis or  
; TITLE OF INVENTION: therapeutic treatment of multiple sclerosis  
; FILE REFERENCE: 2784 PTWO  
; CURRENT APPLICATION NUMBER: US/10/482,044  
; CURRENT FILING DATE: 2003-12-22  
; PRIOR APPLICATION NUMBER: PCT/EP 02/06767  
; PRIOR FILING DATE: 2002-06-19  
; PRIOR APPLICATION NUMBER: FI2001A000114  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 5  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: glycopeptide  
; NAME/KEY: CARBOHYD  
; LOCATION: (2)..(2)  
; OTHER INFORMATION: the carbohydrate is beta-D-glucopyranosyl  
US-10-482-044-5

Query Match 100.0%; Score 94; DB 16; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.6e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
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DB 1 ENPVVHFFKNIVTPRTP 17

RESULT 6  
US-09-740-003-2  
; Sequence 2, Application US/09740003  
; Publication No. US20020039582A1  
; GENERAL INFORMATION:  
; APPLICANT: RAYCHAUDHURI, SYAMAL  
; APPLICANT: RASTETTER, WILLIAM H.  
; APPLICANT: BLACK, AMELIA  
; TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE RESPONSES  
; FILE REFERENCE: 37003/275802



CURRENT APPLICATION NUMBER: US/09/740,003  
CURRENT FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: 09/024,220  
PRIOR FILING DATE: 1998-02-17  
PRIOR APPLICATION NUMBER: 08/476,674  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 08/351,001  
PRIOR FILING DATE: 1994-12-07  
PRIOR APPLICATION NUMBER: 08/919,787  
PRIOR FILING DATE: 1997-08-29  
PRIOR APPLICATION NUMBER: 07/735,069  
PRIOR FILING DATE: 1991-07-25  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 2  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-740-003-2

Query Match 100.0%; Score 94; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.2e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPRTP 17  
Db 2 ENPVVHFFKNIVTPRTP 18

RESULT 7  
US-09-768-872-1  
Sequence 1, Application US/09768872  
Patent No. US20020055466A1  
GENERAL INFORMATION:  
APPLICANT: Anaroni, Rina  
APPLICANT: Teitelbaum, Dvora  
APPLICANT: Arnon, Ruth  
APPLICANT: Sela, Michael  
APPLICANT: Fridkis-Harell, Mashia  
APPLICANT: Strominger, Jack  
TITLE OF INVENTION: Treatment of Autoimmune Conditions with Copolymer 1  
FILE REFERENCE: 1662/493762  
CURRENT APPLICATION NUMBER: US/09/768,872  
CURRENT FILING DATE: 2001-01-23  
PRIOR APPLICATION NUMBER: US 60/093,859  
PRIOR FILING DATE: 1998-07-23  
PRIOR APPLICATION NUMBER: US 60/101,825  
PRIOR FILING DATE: 1998-09-25  
PRIOR APPLICATION NUMBER: US 60/102,960  
PRIOR FILING DATE: 1998-10-02  
PRIOR APPLICATION NUMBER: US 60/106,350  
PRIOR FILING DATE: 1998-10-30  
PRIOR APPLICATION NUMBER: US 60/108,184  
PRIOR FILING DATE: 1998-11-12  
PRIOR APPLICATION NUMBER: US 60/123,675  
PRIOR FILING DATE: 1999-03-09  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: WordPerfect 8.0 for Windows  
SEQ ID NO 1  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic peptide (MBP residues 84-102)  
US-09-768-872-1

Query Match 100.0%; Score 94; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.2e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPRTP 17  
Db 2 ENPVVHFFKNIVTPRTP 18

RESULT 8  
US-09-766-378A-32  
Sequence 32, Application US/09766378A  
Patent No. US20020091079A1  
GENERAL INFORMATION:  
APPLICANT: Rhode, Peter R.  
Acevedo, Jorge  
Burkhardt, Martin  
Jiao, Jin-an  
Wong, Hing C.  
TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/766,378A  
FILING DATE: 19-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/960,190  
FILING DATE: 29-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Corleese, Peter F.  
REGISTRATION NUMBER: 33,860  
REFERENCE/DOCKET NUMBER: 48002-DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-09-766-378A-32

Query Match 100.0%; Score 94; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.2e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPRTP 17  
Db 2 ENPVVHFFKNIVTPRTP 18

RESULT 9  
US-10-239-313A-143  
Sequence 143, Application US/10239313A  
Publication No. US20030175285A1  
GENERAL INFORMATION:  
APPLICANT: KLINGUER - HAMOUR, Christine  
APPLICANT: CORVAIA, Nathalie  
APPLICANT: BECK, Alain

APPLICANT: GOETSCH, Liliane  
TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM  
OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID  
FILE REFERENCE: 343 727 - US  
CURRENT APPLICATION NUMBER: US/10/239,313A  
CURRENT FILING DATE: 2002-09-19  
PRIOR APPLICATION NUMBER: FR 00/03711  
PRIOR FILING DATE: 2000-03-23  
PRIOR APPLICATION NUMBER: PCT 01/70772  
PRIOR FILING DATE: 2001-03-22  
NUMBER OF SEQ ID NOS: 697  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 143  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-239-313A-143

Query Match 100.0%; Score 94; DB 14; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5,2e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPRTP 17  
Db 1 ENPVVHFFKNIVTPRTP 17

RESULT 10  
US-10-743-398-2  
Sequence 2, Application US/10743398  
Publication No. US2004019731A1  
GENERAL INFORMATION:  
APPLICANT: RAYCHAUDHURI, SYAMAL  
APPLICANT: RASTETTER, WILLIAM H.  
APPLICANT: BLACK, AMELIA  
TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE RESPONSES  
FILE REFERENCE: 37003/307430  
CURRENT APPLICATION NUMBER: US/10/743,398  
CURRENT FILING DATE: 2003-12-23  
PRIOR APPLICATION NUMBER: 09/740,003  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: 09/024,220  
PRIOR FILING DATE: 1998-02-17  
PRIOR APPLICATION NUMBER: 08/476,674  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 08/351,001  
PRIOR FILING DATE: 1994-12-07  
PRIOR APPLICATION NUMBER: 08/919,787  
PRIOR FILING DATE: 1997-08-29  
PRIOR APPLICATION NUMBER: 07/735,069  
PRIOR FILING DATE: 1991-07-25  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
peptide  
US-10-743-398-2

Query Match 100.0%; Score 94; DB 16; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5,2e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPRTP 17  
Db 2 ENPVVHFFKNIVTPRTP 18

RESULT 11

US-09-766-378A-28  
Sequence 28, Application US/09766378A  
Patent No. US20020091079A1  
GENERAL INFORMATION:  
APPLICANT: Rhode, Peter R.  
Acavedo, Jorge  
Burkhardt, Martin  
Jiao, Jin-an  
Wong, Hing C.  
TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND  
METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: usa  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/766,378A  
FILING DATE: 19-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/960,190  
FILING DATE: 28-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Corleiss, Peter F.  
REGISTRATION NUMBER: 33,860  
REFERENCE/DOCKET NUMBER: 48002-DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 28:  
US-09-766-378A-28

Query Match 100.0%; Score 94; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5,5e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPRTP 17  
Db 3 ENPVVHFFKNIVTPRTP 19

RESULT 12  
US-09-836-433-30  
Sequence 30, Application US/09836433  
Publication No. US20030049797A1  
GENERAL INFORMATION:  
APPLICANT: Yuki, Yoshikazu  
APPLICANT: Uda, Shigezo  
TITLE OF INVENTION: HYBRID PROTEINS FOR AUTOIMMUNE DISEASE  
FILE REFERENCE: NO. US20030049797A1 Assigned  
CURRENT APPLICATION NUMBER: US/09/836,433  
CURRENT FILING DATE: 2001-04-16  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 30  
LENGTH: 20

SQL Sequence 17 AA;

Query Match 100.0%; Score 94; DB 7; Length 17;

Best Local Similarity 100.0%; Pred. No. 6.1e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
1 ENPVVHFFKNIVTPRTP 17

DB 1 ENPVVHFFKNIVTPRTP 17

RESULT 9

ADK67704

ID ADK67704 standard; peptide; 17 AA.

AC ADK67704;

XX 06-MAY-2004 (first entry)

DE Human myelin basic protein peptide fragment MBP-1 (aa110-126).

KW Human; myelin basic protein; vaccine; multiple sclerosis; T cell.

XX Homo sapiens.

XX WO2004015070-A2.

XX 19-FEB-2004.

XX 06-AUG-2003; 2003WO-US024548.

XX 08-AUG-2002; 2002US-0402521P.

XX (BAYU ) BAYLOR COLLEGE MEDICINE.

XX (OPEX-) OPEXA PHARM INC.

XX Zhang JZ;

XX WPI; 2004-180654/17.

PT Isolating one or more T cells specific for an antigen of interest  
PT comprises incubating a T cell sample with an antigen, useful for  
PT diagnosing or treating multiple sclerosis, psoriasis, thyroiditis,  
PT diabetes and rheumatoid arthritis.

PS Example 1; SEQ ID NO 1; 38pp; English.

CC The present invention is direct to methods of isolating antigen specific  
CC T cells, especially T cells specific for self or autoantigens. This  
CC comprises incubating a sample of T cells obtained from a patient with the  
CC antigen and selecting T cells that express one or more of first markers  
CC selected from CD69, CD4, CD25, CD36 and HLA-DR, and one or more second  
CC markers selected from interleukin-2, interferon-gamma, tumour necrosis  
CC factor alpha, interleukin-5, interleukin-10 and interleukin-12. The  
CC methods are useful for isolating autoreactive T cells which play a role  
CC in the pathogenesis of autoimmune diseases. The methods also permit the  
CC diagnosis of autoimmune disease as well as monitoring the progression of  
CC the disease and for monitoring the efficacy of treatment. The methods of  
CC allow the preparation of autologous T cell vaccines for the treatment of  
CC T cell related autoimmune diseases. Vaccine preparation involves the  
CC isolation of antigen-specific T cells optionally followed by culturing  
CC specific T cells. The expansion of the population of isolated antigen-  
CC specific T cells. An example from the invention describes the isolation  
CC of myelin-reactive T cells for T cell vaccination. Peripheral blood  
CC mononuclear cells were isolated from the blood of multiple sclerosis  
CC patients and incubated with peptides comprising known immunodominant  
CC regions of 3 myelin proteins. These included the present peptide, which  
CC comprises amino acids 110-126 of human myelin basic protein. Cells were  
CC then selected for the expression of gene products indicative of activated  
CC T cells, and myelin-reactive T cells were propagated in culture. The  
CC methods and compositions of the invention are useful for the diagnosis  
CC and/or treatment of autoimmune diseases or T cell associated conditions  
CC such as multiple sclerosis, myasthenia gravis, psoriasis, systemic lupus

CC erythematous, autoimmune thyroiditis, Grave's disease, inflammatory  
CC bowel disease, diabetes and rheumatoid arthritis.

SQL Sequence 17 AA;

Query Match 100.0%; Score 94; DB 8; Length 17;

Best Local Similarity 100.0%; Pred. No. 6.1e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
1 ENPVVHFFKNIVTPRTP 17

DB 1 ENPVVHFFKNIVTPRTP 17

RESULT 10

ADL18291

ID ADL18291 standard; peptide; 17 AA.

XX ADL18291;

XX 20-MAY-2004 (first entry)

DE Human myelin basic protein (MBP), peptide #2.

KW Demyelinating disease; neuron-specific antigen; human;

KW myelin basic protein; MBP; myelin oligodendrocyte glycoprotein;

KW myelin associated glycoprotein; MAG; proteolipid protein; PLP;

KW small heat shock protein; transaldolase; glial fibrillary protein;

KW S-100 protein; cross-reactive peptide; glutamate receptor;

KW phosphodiesterase; multiple sclerosis.

XX Homo sapiens.

XX US2004043431-A1.

XX 04-MAR-2004.

XX 29-AUG-2002; 2002US-00233892.

XX 29-AUG-2002; 2002US-00233892.

XX (VOUD/) VOUDANT A.

XX Vojdani A;

XX WPI; 2004-313756/29.

PT Diagnosing likelihood and severity of demyelinating disease, by  
PT determining antibodies against neuron-specific antigen, comparing level  
PT of detected antibodies with normal level for detecting absence/likelihood  
PT of demyelinating disease.

PS Claim 6; SEQ ID NO 2; 27pp; English.

CC The present invention relates to a method of diagnosing the likelihood  
CC and severity of demyelinating diseases. The method involves determining  
CC antibodies against neuron-specific antigen in sample, comparing the level  
CC of antibodies with the normal level of antibodies, where normal level of  
CC antibodies for neuron-specific antigen indicate optimal conditions, lower  
CC than or higher than normal level of antibodies for the antigen indicate  
CC an absence of or a likelihood of demyelinating diseases, respectively.  
CC The neuron-specific antigen is chosen from myelin basic protein (MBP),  
CC myelin oligodendrocyte glycoprotein, myelin associated glycoprotein  
CC (MAG), proteolipid protein (PLP), small heat shock protein,  
CC transaldolase, glial fibrillary protein, S-100 protein, cross-reactive  
CC peptide from dietary protein, cross-reactive peptide from infectious  
CC agent, glutamate receptor, and phosphodiesterase. The immunoassay is an  
CC enzyme linked immunosorbent assay (ELISA) test. The method is useful for  
CC diagnosing the likelihood and severity of demyelinating diseases such as  
CC multiple sclerosis in a patient. The present sequence represents a  
CC peptide from human MBP.

SQL Sequence 17 AA;

Query Match 100.0%; Score 94; DB 8; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
| | | | | | | | | | | | | | | | | | |  
DB 1 ENPVVHFFKNIVTPRTP 17

## RESULT 11

AAR44115  
ID AAR44115 standard; peptide; 18 AA.

XX AAR44115;

XX 25-MAR-2003 (revised)

DT 09-MAY-1994 (first entry)

XX Human myelin basic protein residues 85-102.

XX hMBP; suppression; auto immune response; multiple sclerosis;  
KW immunodominant epitope; T-cell proliferation; CD4; T-cells.

XX Homo sapiens.

OS WO9321222-A1.

XX 28-OCT-1993.

XX 09-APR-1993; 93WO-US003369.

XX 09-APR-1992; 92US-00865318.

XX (AUTO-) AUTOIMMUNE INC.

XX Weiner HL, Haefler DA, Miller A, Al-Sabbagh A;

XX WPI; 1993-351657/44.

XX New peptide(s) derived from human myelin basic protein - used for  
PT suppressing auto-immune response, partic. in treating multiple sclerosis.

XX Claim 1; Page 29; 118pp; English.

XX The peptide represents residues 85-102 of human myelin basic protein  
CC (hMBP). The fragment comprises an immunodominant epitope of hMBP which  
CC was identified by overlapping 20-mer oligopeptide sequence analysis using  
CC T-cell line assays. The peptide can be used to stop proliferation of  
CC human T-cells specific for MBP or to elicit active suppression of such T-  
CC cells. They are also used partic. for the treatment of multiple  
CC sclerosis. The peptide is also useful for identifying CD4+ T-cells  
CC reactive with MBP. See also AAR44114-25. (Updated on 25-MAR-2003 to  
CC correct PN field.)

XX Sequence 18 AA;

Query Match 100.0%; Score 94; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.5e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
| | | | | | | | | | | | | | | | | | |  
DB 1 ENPVVHFFKNIVTPRTP 17

## RESULT 12

AAR95357  
ID AAR95357 standard; peptide; 18 AA.

XX AAR95357;

DT 16-DEC-1996 (first entry)

XX Residues 83-100 of myelin basic protein.

DE Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE;  
XX CD4+ T-cell; autoimmune disease; demyelination; central nervous system;  
KW CNS; animal model; human; multiple sclerosis; MS; mammal; benign MS; MOG;  
KW relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP;  
KW diabetes; Graves disease; myasthenia gravis; Good Pasture's syndrome;  
KW psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG;  
KW myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.

XX Synthetic.

XX WO9612737-A2.

XX 02-MAY-1996.

XX 25-OCT-1995; 95WO-US013682.

XX 25-OCT-1994; 94US-00328224.

XX 15-MAR-1995; 95US-00404228.

XX (IMMU-) IMMUNOLOGIC PHARM CORP.

XX Smilek D, Samson M, Gelfer M, Hsu D, Shi J, Paliard X, Devaux B;

XX Rottbard J, Franzen H;

XX WPI; 1996-230552/23.

XX Myelin basic derived peptide(s) and analogs - used in the treatment of  
PT Multiple Sclerosis, psoriasis, Graves Disease, etc.

XX Claim 8; Fig 14; 91pp; English.

XX AAR95334-R95374 represent peptides derived from myelin basic protein  
CC (MBP). Immunisation with MBP can be used to induce experimental allergic  
CC encephalomyelitis (EAE) in susceptible strains of mice. EAE is a CD4+ T-  
CC cell mediated autoimmune disease which results in demyelination of the  
CC central nervous system, resulting in paralysis and other neurological  
CC abnormalities. EAE is a commonly used animal model for human multiple  
CC sclerosis (MS). These sequences can be used in compositions for treating  
CC MS in a mammal. The composition acts to down regulate the autoimmune  
CC response, and may be administered in an amount sufficient to prevent the  
CC onset of symptoms of MS. The compositions may also be used to treat  
CC advanced stage MS, especially relapsing-remitting MS, chronic progressive  
CC MS or benign MS. These peptides may also be used in the treatment of  
CC other diseases involving myelin autoantigens, including diabetes, Graves  
CC disease, myasthenia gravis, Good Pasture's syndrome, psoriasis,  
CC thyroiditis, and rheumatoid arthritis. Peptides derived from other myelin  
CC autoantigens, such as myelin oligodendrocyte protein (MOG), proteolipid  
CC protein (PLP), and myelin associated glycoprotein (MAG) can be used as  
CC alternatives to these MBP peptides in these compositions

XX Sequence 18 AA;

Query Match 100.0%; Score 94; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.5e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
| | | | | | | | | | | | | | | | | | |  
DB 1 ENPVVHFFKNIVTPRTP 17

## RESULT 13

AAW73600  
ID AAW73600 standard; peptide; 18 AA.

XX AAW73600;

DT 18-MAR-1999 (first entry)

DE Human myelin basic protein fragment.

XX Myelin basic protein; MBP; human; immunodominant region; inhibitor;  
KW immunosuppressant agent; multiple sclerosis; T cell proliferation;  
KV suppressor inducer.  
XX  
OS Homo sapiens.  
XX  
PN US5858960-A.  
XX  
PD 12-JAN-1999.  
XX  
PF 06-JUN-1995; 95US-00468540.  
XX  
PR 30-MAR-1990; 90US-00502559.  
XX 28-FEB-1992; 92US-00843752.  
PR 09-APR-1992; 92US-00865318.  
PR 09-APR-1993; 93US-00046354.  
XX  
PA (AUTO-) AUTOIMMUNE INC.  
XX  
PI Miller A, Weiner HL, Hafler DA, Al-Sabbagh A;  
XX  
DR MPI; 1999-119958/10.  
XX  
PT New peptides from immunodominant regions of human myelin basic protein -  
XX useful as immunosuppressants for treatment of multiple sclerosis.  
PS  
SQ Claim 1; Col 37; 32pp; English.  
XX  
CC This sequence represents a fragment of the human myelin basic protein  
CC (MBP). The peptides are immunodominant regions of MBP, and are used as  
CC the immunosuppressant agents of the invention. The peptides act on the  
CC response to MBP (or tissues containing it), specifically for treatment of  
CC multiple sclerosis (MS). They either induce energy in MBP-reactive T  
CC cells or actively suppress these cells by inhibiting their proliferation,  
CC possibly by inducing suppressor T cells. The peptides may also be used to  
CC detect specific T cells. The MBP fragments do not induce 'global'  
CC immunosuppression upon prolonged use (increasing the risk of a patient  
CC developing certain malignancies), will not down regulate normal immune  
CC responses to pathogenic micro-organisms and are less toxic than drugs  
CC currently used for the treatment of MS, such as azathioprine (Imuran),  
CC and cyclosporin A  
CC  
XX  
SQ Sequence 18 AA;  
XX  
Query Match 100.0%; Score 94; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.5e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
DB 1 ENPVVHFFKNIVTPRTP 17  
XX  
RESULT 14  
ID AAY6553 standard; peptide; 18 AA.  
XX  
AC AAY6553;  
XX  
DT 21-MAR-2000 (first entry)  
XX  
DE Myelin basic protein fragment MBP(85-102).  
XX  
KM Myelin basic protein; MBP; autoimmune mediated demyelinating disease;  
KW multiple sclerosis; encephalomyelitis; immune response; human.  
XX  
OS Synthetic.  
XX  
PN Homo sapiens.  
XX  
PN WO957241-A2.  
XX  
PD 11-NOV-1999.  
XX

XX  
PF 05-MAY-1999; 99WO-US009930.  
XX  
PR 05-MAY-1998; 98US-00073109.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Arimilli S, Deshpande S;  
XX  
DR MPI; 2000-072228/06.  
XX  
PT Novel peptides for treating autoimmune diseases of central nervous system  
XX characterized by demyelination.  
XX  
PS Example 1; Fig 1A; 57pp; English.  
XX  
CC The invention provides novel peptides derived from human myelin basic  
CC protein having an amino acid sequence Phe-X-Lys-Asn-Ile-Val-X-X-X-Thr-X-  
CC X, where X is any amino acid. The MBP peptides are used in the treatment  
CC of autoimmune mediated demyelinating disease like multiple sclerosis or  
CC the murine demyelinating experimental autoimmune encephalomyelitis. The  
CC therapeutic compositions comprising novel MBP peptides are used for  
CC inducing oral tolerance or general tolerance. The compositions are used  
CC to downregulate or eliminate autoreactive components of the immune system  
CC and treat autoreactive demyelinating, T-cell mediated immune response.  
CC The novel MBP peptides when administered into a subject are useful for  
CC inhibiting a T-cell mediated immune response against MBP, to treat the T-  
CC cell mediated immune response which causes a pathological condition of  
CC the nervous system e.g., multiple sclerosis. Prevention or suppression of  
CC MHC-restricted immune responses is done without any undesirable side  
CC effects, such as non-specific suppression of an individual's overall  
CC immune response. The MBP peptides provide a safer and more effective  
CC treatment by selectively suppressing autoimmune responses at the helper  
CC CD4+ T-cell levels. Sequences AAY6553-553 represent MBP peptides  
XX  
SQ Sequence 18 AA;  
XX  
Query Match 100.0%; Score 94; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.5e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
DB 1 ENPVVHFFKNIVTPRTP 17  
XX  
RESULT 15  
ID AAR32295 standard; protein; 19 AA.  
XX  
AC AAR32295;  
XX  
DT 25-MAR-2003 (revised)  
XX  
DT 31-MAY-1993 (first entry)  
XX  
DE Sequence of synthetic peptide MBP 84-102 which corresp. to AAs 84-102 of  
XX myelin basic protein.  
XX  
KM Cytotoxin T lymphocyte response; epitope; antigen.  
XX  
OS Synthetic.  
XX  
PN WO9301831-A1.  
XX  
PD 04-FEB-1993.  
XX  
PF 24-JUL-1992; 92WO-US006193.  
XX  
PR 25-JUL-1991; 91US-00735069.  
XX  
PA (IDEC-) IDEC PHARM CORP.  
XX  
PI Raychaudhuri S, Rastetter WH;  
XX

XX WPI, 1993-058526/07.  
DR  
XX  
XX New compsn. comprising an antigen and a formulation - to induce a  
PT cytotoxic T-lymphocyte response, useful for treating malaria, HIV,  
PT influenza, hepatitis, herpes, cancer, etc.  
XX  
PS Disclosure, Page 19, 56pp, English.  
CC  
XX  
CC Cardone and Bevan demonstrated that cytotoxic T-lymphocyte (CTL) induced  
CC in C57Bl/6 mice by EG7-ova transfectant, and by cytoplasmically ova-  
CC loaded splenocytes recognise E14 cells coated with the peptide ova 258-  
CC 276. To determine whether soluble ovalbumin in AF induces similar CTL  
CC responses, spleen cells were prepared from immunised mice and stimulated  
CC in vitro with EG7-ova. The effectors were tested against E14 cells coated  
CC with the peptide ova 253-276 or with a control peptide derived from  
CC myelin basic protein (MBP 84-102). The results demonstrate that ova-AF  
CC primed CTL with a similar specificity to those primed by transfectants,  
CC or by cytoplasmically loaded ova. (Updated on 25-MAR-2003 to correct FN  
CC field.)  
SQ Sequence 19 AA;

Query Match 100.0%; Score 94; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.9e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 ENPVVHFFKNIVTPRPP 17  
| | | | | | | | | | | | | | | | | | |  
DB 2 ENPVVHFFKNIVTPRPP 18

Search completed: June 7, 2005, 08:56:41  
Job time : 10.6321 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: June 7, 2005, 08:49:07 ; Search time 2.37824 Seconds  
(without alignments)  
533.603 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94

Sequence: 1 ENPVVHFFKNIVTPRTP 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Issued Patents, AA:\*

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- 2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/prodata/1/1aa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/prodata/1/1aa/Backfillseq1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	100.0	17	US-09-137-759-3	Sequence 3, Appli
2	94	100.0	17	US-09-378-244-3	Sequence 3, Appli
3	94	100.0	18	US-08-468-540B-18	Sequence 18, Appli
4	94	100.0	19	US-08-640-344-2	Sequence 2, Appli
5	94	100.0	19	US-08-468-540B-9	Sequence 9, Appli
6	94	100.0	19	US-08-468-540B-17	Sequence 17, Appli
7	94	100.0	19	US-08-468-540B-24	Sequence 24, Appli
8	94	100.0	19	US-08-297-395-1	Sequence 1, Appli
9	94	100.0	19	US-09-024-220-2	Sequence 2, Appli
10	94	100.0	19	US-08-960-190A-32	Sequence 32, Appli
11	94	100.0	19	US-08-449-728-2	Sequence 2, Appli
12	94	100.0	19	US-09-077-028A-15	Sequence 15, Appli
13	94	100.0	19	US-09-740-003-2	Sequence 2, Appli
14	94	100.0	20	US-08-640-344-1	Sequence 1, Appli
15	94	100.0	20	US-08-640-344-3	Sequence 3, Appli
16	94	100.0	20	US-08-640-344-4	Sequence 4, Appli
17	94	100.0	20	US-08-640-344-5	Sequence 5, Appli
18	94	100.0	20	US-08-640-344-6	Sequence 6, Appli
19	94	100.0	20	US-08-640-344-7	Sequence 7, Appli
20	94	100.0	20	US-08-640-344-8	Sequence 8, Appli
21	94	100.0	23	US-08-787-547-1	Sequence 1, Appli
22	94	100.0	24	US-08-480-190-46	Sequence 46, Appli
23	94	100.0	24	US-08-488-379-46	Sequence 46, Appli
24	94	100.0	24	US-08-475-399A-46	Sequence 46, Appli
25	94	100.0	24	US-09-339-043D-2501	Sequence 2501, Ap
26	94	100.0	24	US-08-077-255A-46	Sequence 46, Appli
27	94	100.0	24	PCT-US93-07545-46	Sequence 46, Appli

28	94	100.0	40	3	US-08-297-395-2	Sequence 2, Appli
29	94	100.0	168	6	5194425-4	Patent No. 5194425
30	94	100.0	168	6	5194425-4	Patent No. 5194425
31	94	100.0	170	1	US-08-227-372-1	Sequence 1, Appli
32	94	100.0	170	2	US-08-327-357A-1	Sequence 1, Appli
33	94	100.0	170	3	US-08-470-397-1	Sequence 1, Appli
34	94	100.0	170	3	US-09-007-520-1	Sequence 1, Appli
35	94	100.0	170	3	US-08-462-351-3	Sequence 1, Appli
36	94	100.0	170	3	US-09-055-263-1	Sequence 1, Appli
37	94	100.0	170	3	US-09-007-520-1	Sequence 1, Appli
38	94	100.0	170	3	US-08-342-408B-2	Sequence 2, Appli
39	94	100.0	170	4	US-09-602-807-3	Sequence 3, Appli
40	94	100.0	170	6	5194425-3	Patent No. 5194425
41	94	100.0	170	6	5194425-3	Patent No. 5194425
42	94	100.0	171	2	US-08-781-122-2	Sequence 2, Appli
43	94	100.0	171	3	US-09-137-759-2	Sequence 2, Appli
44	94	100.0	171	3	US-08-953-937-2	Sequence 2, Appli
45	94	100.0	171	3	US-09-378-244-2	Sequence 2, Appli

## ALIGNMENTS

```
RESULT 1
US-09-137-759-3
; Sequence 3, Application US/09137759
; Patent No. 6251396
; GENERAL INFORMATION:
; APPLICANT: Gaur, Amitabh
; APPLICANT: Conlon, Paul J.
; APPLICANT: Ling, Nicholas C.
; APPLICANT: Staehlin, Theophil
; APPLICANT: Crowe, Paul D.
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING
; FILE REFERENCE: 690068, 405C1
; CURRENT APPLICATION NUMBER: US/09/137,759
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
US-09-137-759-3
Query Match          100.0%; Score 94; DB 3; Length 17;
Best local Similarity 100.0%; Pred. No. 6.4e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 ENPVVHFFKNIVTPRTP 17
Db       1 ENPVVHFFKNIVTPRTP 17
RESULT 2
US-09-378-244-3
; Sequence 3, Application US/09378244
; Patent No. 6379670
; GENERAL INFORMATION:
; APPLICANT: Gaur, Amitabh
; APPLICANT: Conlon, Paul J.
; APPLICANT: Ling, Nicholas C.
; APPLICANT: Staehlin, Theophil
; APPLICANT: Crowe, Paul D.
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING
; FILE REFERENCE: 690068, 405C2
; CURRENT APPLICATION NUMBER: US/09/378,244
; CURRENT FILING DATE: 1999-08-19
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COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,540B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jacobs, Seth H  
REGISTRATION NUMBER: 32,140  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: NO. 58589806  
US-08-468-540B-9

Query Match 100.0%; Score 94; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
|||  
Db 2 ENPVVHFFKNIVTPRTP 18

RESULT 6  
US-08-468-540B-17  
Sequence 17, Application US/08468540B  
Patent No. 5858980  
GENERAL INFORMATION:  
APPLICANT: Weiner, Howard  
APPLICANT: Hatler, David  
APPLICANT: Miller, Ariel  
APPLICANT: Al-Sabbagh, Ahmad  
TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION  
TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESSES:  
ADDRESSES: Darby & Darby P.C.  
STREET: 805 Third Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,540B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jacobs, Seth H

REGISTRATION NUMBER: 32,140  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: NO. 58589806  
US-08-468-540B-17

Query Match 100.0%; Score 94; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
|||  
Db 2 ENPVVHFFKNIVTPRTP 18

RESULT 7  
US-08-468-540B-24  
Sequence 24, Application US/08468540B  
Patent No. 5858980  
GENERAL INFORMATION:  
APPLICANT: Weiner, Howard  
APPLICANT: Hatler, David  
APPLICANT: Miller, Ariel  
APPLICANT: Al-Sabbagh, Ahmad  
TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION  
TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESSES:  
ADDRESSES: Darby & Darby P.C.  
STREET: 805 Third Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,540B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jacobs, Seth H  
REGISTRATION NUMBER: 32,140  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: NO. 58589806  
US-08-468-540B-24

Query Match 100.0%; Score 94; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPRTP 17  
Db 2 ENPVVHFFKNIVTPRTP 18

RESULT 8  
US-08-297-395-1

; Sequence 1, Application US/08297395A  
; Patent No. 6039947

; GENERAL INFORMATION:

; APPLICANT: Howard L. Weiner

; APPLICANT: David A. Hafler

; TITLE OF INVENTION: PEPTIDES DERIVED FROM IMMUNODOMINANT

; FILE REFERENCE: 1010/05723US3

; CURRENT APPLICATION NUMBER: US/08/297,395A

; EARLIER FILING DATE: 1994-08-11

; EARLIER APPLICATION NUMBER: 08/059,189

; EARLIER FILING DATE: 1993-05-06

; EARLIER APPLICATION NUMBER: 07/502,559

; EARLIER FILING DATE: 1990-03-30

; EARLIER APPLICATION NUMBER: PCT/US88/02139

; EARLIER FILING DATE: 1988-06-24

; EARLIER APPLICATION NUMBER: 07/065,734

; EARLIER FILING DATE: 1987-06-24

; NUMBER OF SEQ ID NOS: 84

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 19

; TYPE: PRT

; ORGANISM: Homo sapiens

US-08-297-395-1

Query Match 100.0%; Score 94; DB 3; Length 19;

Best Local Similarity 100.0%; Pred. No. 7.2e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPRTP 17  
Db 2 ENPVVHFFKNIVTPRTP 18

RESULT 9  
US-09-024-220-2

; Sequence 2, Application US/09024220

; Patent No. 6197311

; GENERAL INFORMATION:

; APPLICANT: RAYCHAUDHURI, Syamal

; APPLICANT: RASTETTER, William H.

; APPLICANT: BLACK, Amelia

; TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE

; RESPONSES

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; APPLICATION DATA:

; APPLICATION NUMBER: US/09/024,220

; FILING DATE: 17-Feb-1998

; CLASSIFICATION: <Unknown>

; 24-JUL-1992

25-JUL-1991  
PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/476,674

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 07/919,787

; FILING DATE: 24-JUL-1992

; APPLICATION NUMBER: US 07/735,069

; FILING DATE: 25-JUL-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Teekin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-149

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 19 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-024-220-2

Query Match 100.0%; Score 94; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPRTP 17  
Db 2 ENPVVHFFKNIVTPRTP 18

RESULT 10  
US-08-960-190A-32

; Sequence 32, Application US/08960190A

; Patent No. 6232445

; GENERAL INFORMATION:

; APPLICANT: Rhode, Peter R.

; APPLICANT: Acevedo, Jorge

; APPLICANT: Burkhardt, Martin

; APPLICANT: Jiao, Jin-an

; APPLICANT: Wong, Hing C.

; TITLE OF INVENTION: SOLUBLE HMG COMPLEXES AND

; TITLE OF INVENTION: METHODS OF USE THEREOF

; NUMBER OF SEQUENCES: 38

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP

; STREET: 130 Water Street

; CITY: Boston

; STATE: MA

; COUNTRY: usa

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/960,190A

; FILING DATE: 29-OCT-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Cortes, Peter P

; REGISTRATION NUMBER: 33,860

; REFERENCE/DOCKET NUMBER: 48002

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-523-3400

; TELEFAX: 617-523-6440

TELEX:  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-960-190A-32

Query Match 100.0%; Score 94; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPRTP 17  
Db 2 ENPVVHFFKNIVTPRTP 18

RESULT 11

US-08-449-728-2  
; Sequence 2, Application US/08449728  
; Patent No. 6270769

GENERAL INFORMATION:  
; APPLICANT: STAMAL RAYCHAUDHURI  
; APPLICANT: WILLIAM H. RASTETTER  
; TITLE OF INVENTION: INDUCTION OF CYTOTOXIC  
; TITLE OF INVENTION: T-LYMPHOCYTE RESPONSES  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90017

COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM PS/2 Model 502 or 555X  
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
; SOFTWARE: Wordperfect (Version 5.0)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/449,728

FILING DATE:

CLASSIFICATION:

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/735,069  
; FILING DATE: 25-JUL-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 194/160  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-449-728-2

Query Match 100.0%; Score 94; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPRTP 17  
Db 2 ENPVVHFFKNIVTPRTP 18

RESULT 12  
US-09-077-028A-15  
; Sequence 15, Application US/09077028A  
; Patent No. 6531133  
; GENERAL INFORMATION:  
; APPLICANT: HAYA LOREBERGOM-GALSKI  
; APPLICANT: IDA STEINBERGER  
; APPLICANT: EVELINE BERAUD  
; APPLICANT: IRINA MARIANOVSKY  
; APPLICANT: SHAI YARKONI  
; TITLE OF INVENTION: PSEUDOMONAS EXOTOXIN-MYELIN BASIC PROTEIN CHIMERIC  
; FILE REFERENCE: LOREBERGOM-1  
; CURRENT APPLICATION NUMBER: US/09/077,028A  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR FILING DATE: 1995-11-17  
; PRIOR FILING DATE: 1995-11-17  
; PRIOR FILING DATE: 1995-12-26  
; PRIOR FILING DATE: 1995-12-26  
; PRIOR FILING DATE: 1996-11-17  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-077-028A-15

Query Match 100.0%; Score 94; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPRTP 17  
Db 2 ENPVVHFFKNIVTPRTP 18

RESULT 13

US-09-740-003-2  
; Sequence 2, Application US/09740003  
; Patent No. 6733763  
; GENERAL INFORMATION:  
; APPLICANT: RAYCHAUDHURI, SYAMAL  
; APPLICANT: RASTETTER, WILLIAM H.  
; APPLICANT: BLACK, AMELIA  
; TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE RESPONSES  
; FILE REFERENCE: 37003/275802  
; CURRENT APPLICATION NUMBER: US/09/740,003  
; CURRENT FILING DATE: 2000-12-20  
; PRIOR FILING DATE: 1998-02-17  
; PRIOR FILING DATE: 1998-02-17  
; PRIOR FILING DATE: 1998-02-17  
; PRIOR FILING DATE: 1998-02-17  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/351,001  
; PRIOR FILING DATE: 1994-12-07  
; PRIOR APPLICATION NUMBER: 08/919,787  
; PRIOR FILING DATE: 1997-08-29  
; PRIOR APPLICATION NUMBER: 07/735,069  
; PRIOR FILING DATE: 1991-07-25  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-09-740-003-2

Query Match 100.0%; Score 94; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ENPVVHFFKNIIVTPRTP 17
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Db      2 ENPVVHFFKNIIVTPRTP 18
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RESULT 14  
US-08-640

US-08-640-344-1  
; Sequence 1, Application US/08640344  
; Patent No. 5824315  
GENERAL INFORMATION:

```

; GENERAL INFORMATION:
; APPLICANT: NAG, BISHWAJIT

```

APPLICANT: MUKKU, PRABHA

APPLICANT: DESHPANDE, SHRIKANT  
TITLE OF INVENTION: IMPROVING BINDING AFFINITY OF ANTIGENIC  
PEPTIDES FOR MHC MOLECULES

```

; TITLE OF INVENTION: PEPTIDES FOR MHC MOLECULES
; NUMBER OF SEQUENCES: 18
; CONTACT INFORMATION:

```

CORRESPONDENCE ADDRESS: ADDRESS: TOWN/END

ADDRESS: JONNSEND & CREW BLVD  
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
CITY: SAN FRANCISCO

STATE: CALIFORNIA  
COUNTRY: U S A

ZIP: 94111-3834

```
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY
```

COMPUTER: IBM PC compatible

```

;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/640,344
;

```

! FILING DATE: 30-APR-1996  
! CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: STORELLA ESQ., JOHN R.

REGISTRATION NUMBER: 32,944  
REFERENCE NUMBER: 14058-004800

TELECOMMUNICATION INFORMATION  
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE AND COMMENTARY

SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids

TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: 1 in 2

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; 10F0D081: linear
; MOLECULE TYPE: peptide
; ;
; 11E-08-640-344-1

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03-V8-030-333-1

Query match	100.0%	Score 94	DB 2	Length 20
Best Local Similarity	100.0%	Pred. NO.	7.6e-09	
Matches 17	Conservative	0	Mismatches	0
			Gaps	0

Qy	1	ENPVVHFFKNI	VT	PR	TP	17
Db	3	ENPVVHFFKNI	VT	PR	TP	19

## RESULT 15

US-08-640-344-3  
; Sequence 3, Application US/08640344

; Patent No. 5824315  
; GENERAL INFORMATION:

APPLICANT: NAG, BISHWAJIT  
APPLICANT: MUKKU, PRABHA

APPLICANT: DESHPANDE, SHRIKANT  
TITLE OF INVENTION: IMPROVING BINDING AFFINITY OF ANTIGENIC

; TITLE OF INVENTION: PEE  
 ; NUMBER OF SEQUENCES: 18  
 ;

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP  
; ;

STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
CITY: SAN FRANCISCO

```

STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,344
FILING DATE: 30-APR-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STORELLA ESQ., JOHN R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 14058-004800
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ. ID NO.: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide

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Query Match      100.0%; Score 94; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 7 6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 ENPVVHFFKNI VTP RTP 17
        |||||
Db      3 ENPVVHFFKNI VTP RTP 19
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Search completed: June 7, 2005, 09:04:02  
Job time : 3.37824 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 09:33:36 ; Search time 38 Seconds  
(without alignments)  
43.044 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94

Sequence: 1 ENPVVHFFKNIVTPRTP 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 2991

Minimum DB seq length: 0  
Maximum DB seq length: 17  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	45.7	14	2 S12904	protein kinase (EC
2	24	25.5	11	2 A54348	N-acetylglucosamin
3	24	25.5	16	2 S03405	hydrogenase (EC 1.
4	24	25.5	16	2 A59046	alpha-conotoxin M1
5	23	24.5	9	2 S55696	phosphoenolpyruvat
6	23	24.5	14	2 PH1628	Ig H chain V-D-J r
7	23	24.5	16	2 S65520	phospholipase A2 (
8	22	23.4	10	2 A58365	neuropeptide FFRa
9	22	23.3	7	2 S42620	aggreccan - bovine
10	21	22.3	15	2 S62641	porphobilinogen by
11	20	21.3	10	2 A43977	FMRFamide-like pro
12	20	21.3	13	2 PH1620	Ig H chain V-D-J r
13	20	21.3	13	2 PC2369	unidentified 85K p
14	20	21.3	14	2 S62374	alpha-1-antichymot
15	20	21.3	15	2 A35417	28k serine protein
16	20	21.3	16	2 A49255	T-cell receptor be
17	20	21.3	16	2 PH1640	Ig H chain V-D-J r
18	20	21.3	16	2 S09084	procaseome chain 3
19	19.5	20.7	9	2 PT0080	60K Ca binding pro
20	19	20.2	12	2 PQ0730	unidentified 5.4/3
21	19	20.2	13	2 PH1593	Ig H chain V-D-J r
22	19	20.2	13	2 A61514	glutathione transf
23	19	20.2	15	2 B61457	protein 425 - Cal
24	19	20.2	15	2 G60977	formate dehydrogen
25	19	20.2	15	2 S59492	emiatin synthetas
26	19	20.2	15	2 PA0093	ribosomal protein
27	19	20.2	16	2 A28144	transforming prote
28	19	20.2	16	2 A46236	hypothetical prote
29	19	20.2	16	2 S42237	

30	19	20.2	16	2 B48406	annexin VI homolog
31	19	20.2	17	2 S32587	L-ascorbate peroxi
32	18	19.1	8	2 B39745	endoglycosylcerami
33	18	19.1	11	2 C61497	seed protein ws-18
34	18	19.1	11	4 PC2390	trichotozin I - fu
35	18	19.1	11	4 PC2392	trichotozin III -
36	18	19.1	12	2 B39690	neural cell adhesi
37	18	19.1	13	1 UNB0	neurotensin - bovi
38	18	19.1	13	2 A33208	calreticulin, hepa
39	18	19.1	13	2 A40207	cell surface glyco
40	18	19.1	14	2 S29632	xylan 1,4-beta-xy
41	18	19.1	14	2 S59495	formate dehydrogen
42	18	19.1	14	2 A60158	disaggregatase - M
43	18	19.1	14	2 B56884	Pax-QNR, long form
44	18	19.1	15	2 B33208	calreticulin, uter
45	18	19.1	15	2 S27248	pseudogermin - whe

## ALIGNMENTS

RESULT 1  
S12904  
protein kinase (EC 2.7.1.37) - scarfish (Pisaster ochraceus)  
C/Species: Pisaster ochraceus  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #ext\_change 09-Jul-2004  
C/Accession: S12904  
R/Sanger, J.S.; Aebersold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L.  
FEBS Lett. 273, 223-226, 1990  
A/Title: Identification of the sites in myelin basic protein that are phosphorylated by n  
A/Reference number: S12904; WUID:91032186; PMID:1699809  
A/Accession: S12904  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-14 <SN>  
A/Cross-references: UNIPROT:Q7M3W4  
C/Keywords: phosphotransferase

Query Match  
Best Local Similarity 100.0%; Pred. No. 0.41;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NIVTPRTP 17  
Db 1 NIVTPRTP 8

RESULT 2  
A54348  
N-acetylglucosamine-6-sulfatase (EC 3.1.6.14) - bovine (fragment)  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #ext\_change 05-Jan-1996  
C/Accession: A54348  
R/Shilatifard, A.; Cummings, R.D.  
Biochemistry 33, 4273-4282, 1994  
A/Title: Purification and characterization of N-acetylglucosamine-6-sulfatase frc  
A/Reference number: A54348; WUID:94206936; PMID:8155645  
A/Accession: A54348  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-11 <SHI>  
C/Keywords: sulfuric ester hydrolase

Query Match  
Best Local Similarity 62.5%; Pred. No. 5.5e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 FFKNIWTP 14  
Db 4 FFKNIWTP 11

RESULT 3

S03405  
hydrogenase (EC 1.18.99.1) small chain - Alcaligenes eutrophus (fragment)  
C:Species: Alcaligenes eutrophus  
C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 13-Sep-1998  
C:Accession: S03405  
R:Ioerenz, B.; Schneider, K.; Kretzin, H.; Schlegel, H.G.  
Biochim. Biophys. Acta 995, 1-9, 1989  
A:Title: Immunological comparison of subunits isolated from various hydrogenases of aerc  
A:Reference number: S03404; PMID:89166625; PMID:2493816  
A:Accession: S03405  
A:Molecule type: protein  
A:Residues: 1-16 <LOR>  
A:Experimental source: strain H16, DMS 541  
C:Superfamily: hydrogenase (N1Fe), small chain  
C:Keywords: hydrogen metabolism; iron-sulfur protein; membrane bound; metalloprotein; ni

Query Match  
Best Local Similarity 25.5%; Score 24; DB 2; Length 16;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PRTP 17  
|||  
Db 5 PRTP 8

RESULT 4  
A59046  
alpha-conotoxin MII - cone shell (Conus magus)  
C:Species: Conus magus (magus cone)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C:Accession: A59046  
R:Cartier, G.E.; Yoshikami, D.; Gray, W.R.; Luo, S.; Olivera, B.M.; McIntosh, J.M.  
J. Biol. Chem. 271, 7522-7528, 1996  
A:Title: A new alpha-conotoxin which targets alpha3beta2 nicotinic acetylcholine recept  
A:Reference number: A59046; PMID:96205934; PMID:8631783  
A:Accession: A59046  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-16 <CAR>  
A:Cross-references: UNIPROT:P56636  
C:Superfamily: alpha-conotoxin  
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro  
F:1-16/Product: alpha-conotoxin MII #status experimental <MAT>  
F:2-8,3-16/Dissulfide bonds: #status experimental  
F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match  
Best Local Similarity 25.5%; Score 24; DB 2; Length 16;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPVH 6  
|||  
Db 5 NPVCH 9

RESULT 5  
S55696  
phosphoenolpyruvate carboxykinase - Trypanosoma brucei  
C:Species: Trypanosoma brucei  
C:Date: 28-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: S55696  
R:Hunt, M.; Koehler, P.  
Biochim. Biophys. Acta 1249, 15-22, 1995  
A:Title: Purification and characterization of phosphoenolpyruvate carboxykinase from Try  
A:Reference number: S55696; PMID:95284106; PMID:7766679  
A:Accession: S55696  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <HUN>  
A:Cross-references: UNIPROT:Q7M355

Query Match  
Best Local Similarity 24.5%; Score 23; DB 2; Length 9;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 4; Conservative 3; Mismatches 0; Indels 2; Gaps 1;  
QY 3 PVHFFKNI 11  
|::|::|  
Db 2 PIIH--KNL 8

RESULT 6  
PH1628  
Ig H chain V-D-J region (clone B-1ess 151) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C:Accession: PH1628  
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-1ess mice  
A:Reference number: PH1580; PMID:93301609; PMID:8315387  
A:Accession: PH1628  
A:Molecule type: DNA  
A:Residues: 1-14 <LBV>  
A:Experimental source: bone marrow pre-B lymphocyte  
C:Keywords: immunoglobulin

Query Match  
Best Local Similarity 24.5%; Score 23; DB 2; Length 14;  
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 HFFKNIV 12  
|::|::|  
Db 4 HYNSML 10

RESULT 7  
S65520  
phospholipase A2 (EC 3.1.1.4) - Malayan spitting cobra (fragment)  
N:Contains: muscarinic acetylcholine receptor inhibitor  
C:Species: Naja naja sputatrix (Malayan spitting cobra)  
C:Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 09-Jul-2004  
C:Accession: S65520  
R:Miyaoshi, S.; Tu, A.T.  
Arch. Biochem. Biophys. 328, 17-25, 1996  
A:Title: Phospholipase A2) from Naja naja sputatrix venom is a muscarinic acetylcholine  
A:Reference number: S65520; PMID:96195757; PMID:8638927  
A:Accession: S65520  
A:Molecule type: protein  
A:Residues: 1-16 <MY>  
A:Cross-references: UNIPROT:Q10756  
C:Superfamily: phospholipase A2  
C:Keywords: calcium; carboxylic ester hydrolase; lipid degradation; metalloprotein; presy

Query Match  
Best Local Similarity 24.5%; Score 23; DB 2; Length 16;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 8 FKNIVPRTP 17  
|||::|  
Db 5 FKNVIQCTVP 14

RESULT 8  
A58365  
neuropeptide FRRFamide - blue mussel  
N:Alternate names: FRRFamide-related decapeptide; Mytilus FRRFamide  
C:Species: Mytilus edulis (blue mussel)  
C:Date: 20-Nov-1996 #sequence\_revision 22-Nov-1996 #text\_change 09-Jul-2004  
C:Accession: A58365  
R:Fujisawa, Y.; Ikeda, T.; Nomoto, K.; Yasuda-Kamatani, Y.; Minakata, H.; Kenny, P.T.M.;  
Comp. Biochem. Physiol. C 102, 91-95, 1992  
A:Title: The FRRFamide-related decapeptide of Mytilus contains a D-amino acid residue.  
A:Reference number: A58365; PMID:93047882; PMID:1358533  
A:Accession: A58365  
A:Molecule type: protein  
A:Residues: 1-10 <FUI>

A:Cross-references: UNIPROT:P42560  
A:Experimental source: anterior byssus retractor muscle  
C:Keywords: amidated carboxyl end; D-amino acid; neuropeptide  
F:2/Modified site: D-leucine (Leu) #status experimental  
F:10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 23.4%; Score 22; DB 2; Length 10;  
Best Local Similarity 75.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 HFFK 9  
|||  
Db 6 HFFR 9

RESULT 9  
S42620  
aggrecan - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 19-Mar-1997 #sequence\_revision 24-Jul-1998 #text\_change 24-Jul-1998  
C:Accession: S42620  
R:Vogel, K.G.; Sandy, J.D.; Pogany, G.; Robbins, J.R.  
Matrix Biol. 14, 171-179, 1994  
A:Title: Aggrecan in bovine tendon.  
A:Reference number: S42620; PMID:94340214; PMID:7520336  
A:Accession: S42620  
A:Molecule type: protein  
A:Residues: 1-7 <VOG>  
A:Experimental source: flexor tendon  
C:Keywords: cartilage

Query Match 22.3%; Score 21; DB 2; Length 7;  
Best Local Similarity 80.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 11 IYTPR 15  
|||  
Db 3 IVSPR 7

RESULT 10  
S62641  
porphobilinogen synthase (EC 4.2.1.24) - green alga (Scenedesmus obliquus) (fragment)  
N:Alternate names: 5-aminolevulinic acid dehydratase  
C:Species: Scenedesmus obliquus  
C:Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S62641  
R:Stolz, M.; Doernemann, D.  
Eur. J. Biochem. 236, 600-608, 1996  
A:Title: Purification, metal cofactor, N-terminal sequence and subunit composition of a  
A:Reference number: S62641; PMID:96195670; PMID:8612634  
A:Accession: S62641  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <STO>  
A:Cross-references: UNIPROT:O9S8B1  
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 22.3%; Score 21; DB 2; Length 15;  
Best Local Similarity 80.0%; Pred. No. 2.6e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 11 IYTPR 15  
|||  
Db 11 IVSPR 15

RESULT 11  
A43977  
FMRamide-like protein - tobacco hornworm  
C:Species: Manduca sexta (tobacco hornworm)  
C:Date: 11-Feb-1993 #sequence\_revision 11-Feb-1993 #text\_change 09-Jul-2004  
C:Accession: A43977

R:Kingan, T.G.; Teplow, D.B.; Phillips, J.M.; Riehm, J.P.; Rao, K.R.; Hildebrand, J.G.;  
Peptides 11, 849-856, 1990  
A:Title: A new peptide in the FMRamide family isolated from the CNS of the hawkmoth, Mar

A:Reference number: A43977; PMID:91045350; PMID:2235684  
A:Accession: A43977  
A:Molecule type: protein  
A:Residues: 1-10 <KIN>  
A:Cross-references: UNIPROT:P18523  
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 21.3%; Score 20; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 2.4e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 VVHFF 8  
|||  
Db 3 VVHSF 7

RESULT 12  
PH1620  
Ig H chain V-D-J region (clone B-1ess 40) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C:Accession: PH1620  
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
A:Reference number: PH1580; PMID:93301609; PMID:8315387  
A:Accession: PH1620

A:Molecule type: DNA  
A:Residues: 1-13 <LEU>  
A:Experimental source: bone marrow pre-B lymphocyte  
C:Keywords: immunoglobulin

Query Match 21.3%; Score 20; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 IYTP 14  
|||  
Db 6 IYTP 9

RESULT 13  
PC2369  
unidentified 85k protein [imported] - Bacillus cereus (strain ts-4) (fragment)  
C:Species: Bacillus cereus  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C:Accession: PC2369  
R:Matsumoto, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kaijawa, T.; Hatano, S.  
Biosci. Biotechnol. Biochem. 59, 231-235, 1995  
A:Title: Identification of DNA-binding proteins changed after induction of sporulation in  
A:Reference number: PC2369; PMID:95218265; PMID:776022  
A:Accession: PC2369  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-13 <MAS>  
A:Cross-references: UNIPROT:Q7M0L4

Query Match 21.3%; Score 20; DB 2; Length 13;  
Best Local Similarity 57.1%; Pred. No. 3.2e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 ENPVHAF 7  
|||  
Db 7 ENPWAKF 13

RESULT 14  
S62374

alpha-1-antichymotrypsin - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 24-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S62374  
R:Tsuda, M.; Sei, Y.; Ohkubo, T.; Yamamura, M.; Kamiguchi, H.; Akatsuka, A.; Tsuda, T.;  
Eur. J. Biochem. 235, 821-827, 1996  
A:Title: The defective secretion of a naturally occurring alpha-1-antichymotrypsin varia  
A:Reference number: S62374; MUID:96184564; PMID:8654434  
A:Accession: S62374  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-14 <TSU>  
A:Cross-references: UNIPROT:Q9UNU9; UNIPROT:Q96DW8; UNIPROT:Q8N177

Query Match 21.3%; Score 20; DB 2; Length 14;  
Best Local Similarity 18.2%; Pred. No. 3.5e+03;  
Matches 2; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 5 VHFPEKNIVTPR 15  
:|:|:  
Db 2 IFPMKRVNPK 12

RESULT 15  
A35417  
28K serine proteinase homolog - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 18-Jan-1991 #sequence\_revision 18-Jan-1991 #text\_change 09-Jul-2004  
C:Accession: A35417  
R:Ho, P.L.; Carpenter, M.R.; Smillie, L.B.; Gambardini, A.G.  
Biochem. Biophys. Res. Commun. 170, 769-774, 1990  
A:Title: Co-purification of proteases with basic fibroblast growth factor (bFGF).  
A:Reference number: A35417; MUID:90343797; PMID:220404  
A:Accession: A35417  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <HOA>  
A:Cross-references: UNIPROT:Q7M3G3

Query Match 21.3%; Score 20; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 3.8e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 KNIVTP 14  
|  
Db 10 KGYVTP 15

Search completed: June 7, 2005, 09:37:15  
Job time : 40 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 09:33:36 ; Search time 165 Seconds  
(without alignments)  
52.760 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94

Sequence: 1 ENPVVHFPKNIVTPRTP 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 8390

Minimum DB seq length: 0  
Maximum DB seq length: 17  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	45.7	14	Q7M3M4	Q7M3M4 plasster oc
2	30	31.9	15	Q9BXX4	Q9BXX4 homo sapien
3	30	31.9	15	Q6LCH6	Q6LCH6 mus musculu
4	28	29.8	16	Q8VNS8	Q8VNS8 escherichia
5	27	28.7	15	Q69142	Q69142 streptococ
6	25	26.6	10	Q7RSN9	Q7RSN9 plasmodium
7	25	26.6	12	Q9BY99	Q9BY99 homo sapien
8	25	26.6	12	Q6JC79	Q6JC79 solenodon p
9	25	26.6	12	Q71B00	Q71B00 cynocephalu
10	25	26.6	12	Q71B01	Q71B01 urogale eve
11	25	26.6	12	Q9BFR4	Q9BFR4 manis penta
12	25	26.6	12	Q9BFR5	Q9BFR5 ursus arcto
13	25	26.6	12	Q9BFR6	Q9BFR6 canis fam1
14	25	26.6	12	Q9BFR7	Q9BFR7 panthera on
15	25	26.6	12	Q9BFR8	Q9BFR8 leopardus p
16	25	26.6	12	Q9BFR9	Q9BFR9 felis silve
17	25	26.6	12	Q9BFR0	Q9BFR0 tapirus ind
18	25	26.6	12	Q9BFS1	Q9BFS1 ceratotheri
19	25	26.6	12	Q9BFS2	Q9BFS2 equus cabal
20	25	26.6	12	Q9BFS3	Q9BFS3 okapia john
21	25	26.6	12	Q9BFS4	Q9BFS4 sus scrofa
22	25	26.6	12	Q9BFS5	Q9BFS5 tragelaphus
23	25	26.6	12	Q9BFS6	Q9BFS6 lama glama
24	25	26.6	12	Q9BFS7	Q9BFS7 hippopotamu
25	25	26.6	12	Q9BFS8	Q9BFS8 turipodas tr
26	25	26.6	12	Q9BFS9	Q9BFS9 megaderma n
27	25	26.6	12	Q9BFT0	Q9BFT0 nyctereis th
28	25	26.6	12	Q9BFT1	Q9BFT1 rousettus l
29	25	26.6	12	Q9BFT2	Q9BFT2 pteropus gl
30	25	26.6	12	Q9BFT3	Q9BFT3 artibeus ja
31	25	26.6	12	Q9BFT4	Q9BFT4 callimico g

32	25	26.6	12	2	Q9BFT5	Q9BFT5 macaca mla
33	25	26.6	12	2	Q9BFT6	Q9BFT6 ateles fusc
34	25	26.6	12	2	Q9BFT7	Q9BFT7 tarsius ban
35	25	26.6	12	2	Q9BFT8	Q9BFT8 lemur catca
36	25	26.6	12	2	Q9BFT9	Q9BFT9 cynocephalu
37	25	26.6	12	2	Q9BFT0	Q9BFT0 ochorona hy
38	25	26.6	12	2	Q9BFT1	Q9BFT1 sylviagug
39	25	26.6	12	2	Q9BFT2	Q9BFT2 orycteropus
40	25	26.6	12	2	Q9BFT3	Q9BFT3 elephantulu
41	25	26.6	12	2	Q9BFT4	Q9BFT4 macroscelid
42	25	26.6	12	2	Q9BFT5	Q9BFT5 loxodonta a
43	25	26.6	12	2	Q9BFT6	Q9BFT6 procavia ca
44	25	26.6	12	2	Q9BFT7	Q9BFT7 trichechus
45	25	26.6	12	2	Q9BFT8	Q9BFT8 echinops te

## ALIGNMENTS

RESULT 1					
ID	Q7M3M4	PRELIMINARY:	PRT:	14 AA.	
AC	Q7M3M4:				
DT	01-MAR-2004 (TREMBlrel. 26, Created)				
DT	01-MAR-2004 (TREMBlrel. 26, Last sequence update)				
DT	01-MAR-2004 (TREMBlrel. 26, Last annotation update)				
DE	Protein kinase (EC 2.7.1.37).				
OS	Plasster ochraceus (Sea star).				
OC	Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;				
OC	Asteroidae; Forcipulatacea; Forcipulacida; Asteriidae; Plaster.				
OX	NCBI_Taxid=7612;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=91032186; PubMed=1699809; DOI=10.1016/0014-5793(90)81090-B;				
RA	Sanghera J.S., Aebersold R., Morrison H.D., Bures E.J., Palech S.L.;				
RT	Identification of the sites in myelin basic protein that are				
RT	phosphorylated by meiosis-activated protein kinase p44 (mpk)."				
RL	FEBS Lett. 273:223-226(1990).				
RL	PIR; S12904; S12904.				
DR	GO: GO:0004672; F:protein kinase activity; IEA.				
SO	SEQUENCE 14 AA; 1492 MW; 90BF7368373058171 CRC64;				
Query Match					
		45.7%;	Score 43;	DB 2;	Length 14;
		Best Local Similarity	100.0%;	Pred. No. 4;	
		Matches 8;	Conservative 0;	Mismatches 0;	Indels 0;
		Gaps 0;			
QY	10 NIVTPRTP 17				
DB	1 NIVTPRTP 8				
RESULT 2					
ID	Q9BXX4	PRELIMINARY:	PRT:	15 AA.	
AC	Q9BXX4:				
DT	01-JUN-2001 (TREMBlrel. 17, Created)				
DT	01-JUN-2001 (TREMBlrel. 17, Last sequence update)				
DT	05-JUL-2004 (TREMBlrel. 27, Last annotation update)				
DE	Transcription factor PAX 5 (PAX5) (B-cell specific transcription				
DE	factor) (Fragment).				
GN	Name=PAX5; Synonyms=PAX-5;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Hirabayashi Y., Rahman M., Sasaki T.;				
RL	Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.				
RX	MEDLINE=2154098; PubMed=11460166; DOI=10.1038/35085588;				
RA	Pasqualucci L., Neumeister P., Goossens T., Nanjangud G.,				

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RA Chaganti R.S.K., Koppers R., Dalla-Favera R.;
RT "Hypermutation of multiple proto-oncogenes in B-cell diffuse large-
RL cell lymphomas.";
RN Nature 412:341-346(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=966234102; PubMed=8650231; DOI=10.1073/pnas.93.12.6129;
RA Buslinger M., Kilx N., Pfeiffer P., Graninger P.G., Kozmik Z.;
RT "Deregulation of PAX-5 by translocation of the Emu enhancer of the Igh
RL locus adjacent to two alternative PAX-5 promoters in a diffuse large-
RT cell lymphoma.";
RN Proc. Natl. Acad. Sci. U.S.A. 93:6129-6134(1996).
DR EMBL: AF268279; AAK25737.1; -.
DR EMBL: AF386790; AAK70869.1; -.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1809 MW; 3F95BB53FB3F7A8E CRC64;

Query Match
Best Local Similarity 31.9%; Score 30; DB 2; Length 15;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 KNIVTPRT 16
   |||||
   5 KNVPTPT 12

RESULT 3
O6LCH6 PRELIMINARY; PRT; 15 AA.
AC O6LCH6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE B-cell specific transcription factor (Fragment).
GN Name=PAX-5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=966234102; PubMed=8650231; DOI=10.1073/pnas.93.12.6129;
RA Buslinger M., Kilx N., Pfeiffer P., Graninger P.G., Kozmik Z.;
RT "Deregulation of PAX-5 by translocation of the Emu enhancer of the Igh
RL locus adjacent to two alternative PAX-5 promoters in a diffuse large-
RT cell lymphoma.";
RN Proc. Natl. Acad. Sci. U.S.A. 93:6129-6134(1996).
DR EMBL: U56837; AAB16834.1; -.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1835 MW; 3F95ABE83FB3F7A8E CRC64;

Query Match
Best Local Similarity 31.9%; Score 30; DB 2; Length 15;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 KNIVTPRT 16
   |||||
   5 KNVPTPT 12

RESULT 4
O8VNS8 PRELIMINARY; PRT; 16 AA.
AC O8VNS8;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE Cdc4 protein (Fragment).
GN Name=cdc4;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
```

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OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=413/89-1;
RA Benkel P., Chakraborty T.;
RL Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ277443; CAC81838.1; -.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1826 MW; 0D5EA97E0C676A12 CRC64;

Query Match
Best Local Similarity 29.8%; Score 28; DB 2; Length 16;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTP 14
   |||||
   2 QQPVVVGEMLVTP 15

RESULT 5
O69142 PRELIMINARY; PRT; 15 AA.
AC O69142;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Protein SIC (Fragment).
GN Name=sic;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
RN NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AP1;
RX MEDLINE=98298075; PubMed=9632622;
RA Berge A., Rasmussen M., Bjorck L.;
RT "Identification of an insertion sequence located in a region encoding
RT virulence factors of Streptococcus pyogenes.";
DR EMBL: AF064540; AAC38769.1; -.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1552 MW; 87655FEF847401FF CRC64;

Query Match
Best Local Similarity 28.7%; Score 27; DB 2; Length 15;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 KNIVTPRT 17
   |||||
   4 KPSVTPPT 12

RESULT 6
Q7RSN9 PRELIMINARY; PRT; 10 AA.
AC Q7RSN9;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
GN Name=PY00316;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmidium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Anguioni S.V., Suh B.B., Koof T.W., Perlea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
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RA Shallow S.J., van Aken S.E., Riedmuller S.B., Feldlyum T.V.,
RA Cho J.K., Quackenbush J., Sedegh M., Shoib A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.,
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AABL0100088; EAA22681.1; -.
CC Hypothetical protein.
CC KW
DR EMBL; AABL0100088; EAA22681.1; -.
FT NON TER
SQ SEQUENCE 10 AA; 1209 MW; 3F8986573B42C047 CRC64;

Query Match
Best Local Similarity 26.6%; Score 25; DB 2; Length 10;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPVHFFKNI 8
Db 2 NPVHFFKNI 8

RESULT 7
Q9BY9 PRELIMINARY; PRT; 12 AA.
AC 09BY9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Amyloid beta protein (Fragment).
CN Name:APP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319; DOI=10.1038/35054550;
RX Murphy W.J., Bizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011354; AAG47389.1; -.
FT NON TER
SQ SEQUENCE 12 AA; 1547 MW; 5D6B97CA2D19C9C3 CRC64;

Query Match
Best Local Similarity 26.6%; Score 25; DB 2; Length 12;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NPVHFFKNI 11
Db 1 NPVHFFKNI 10

RESULT 8
Q6JC79 PRELIMINARY; PRT; 12 AA.
AC 06JC79;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE APP (Fragment).
OS Solenodon paradoxus (Hispaniolan solenodon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Solenodontidae; Solenodon.
OX NCB1_TaxID=9805;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RX PubMed=15190349; DOI=10.1038/nature02597;
RX Roca A.L., Bar-Gal G.K., Bizirik E., Helgen K.M., Maria R.,
RA Springer M.S., O'Brien S.J., Murphy W.J.;
RT "Mesozoic origin for West Indian insectivores.";
RL Nature 429:649-651(2004).
DR EMBL; AY530068; AAS67633.1; -.
FT NON TER
SQ SEQUENCE 12 AA; 1547 MW; 5D6B97CA2D19C9C3 CRC64;

Query Match
Best Local Similarity 26.6%; Score 25; DB 2; Length 12;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NPVHFFKNI 11
Db 1 NPVHFFKNI 10

RESULT 9
Q71B00 PRELIMINARY; PRT; 12 AA.
AC 071B00;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE APP (Fragment).
OS Cynocephalus volans (Philippine flying lemur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Dermoptera; Cynocephalidae; Cynocephalus.
OX NCB1_TaxID=110931;
RN [1]
RP SEQUENCE FROM N.A.
RX Bizirik E., Murphy W.J., Springer M.S., O'Brien S.J.;
RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF535039; AAQ10584.1; -.
FT NON TER
SQ SEQUENCE 12 AA; 1547 MW; 5D6B97CA2D19C9C3 CRC64;

Query Match
Best Local Similarity 26.6%; Score 25; DB 2; Length 12;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NPVHFFKNI 11
Db 1 NPVHFFKNI 10

RESULT 10
Q71B01 PRELIMINARY; PRT; 12 AA.
AC 071B01;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE APP (Fragment).
OS Urogale everetti.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupaiidae; Urogale.
OX NCB1_TaxID=192726;
RN [1]
RP SEQUENCE FROM N.A.
RX Bizirik E., Murphy W.J., Springer M.S., O'Brien S.J.;
RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF535038; AAQ10583.1; -.
FT NON TER
SQ SEQUENCE 12 AA; 1547 MW; 5D6B97CA2D19C9C3 CRC64;

Query Match
Best Local Similarity 26.6%; Score 25; DB 2; Length 12;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NPVHFFKNI 11
```

```
Db 1 NPTYKFFEQM 10

RESULT 11
Q9BFR4 PRELIMINARY; PRT; 12 AA.
AC Q9BFR4;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
GN Amyloid beta protein (Fragment).
OS Name=APP;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Pholidota; Manidae; Mania.
RN NCBI_TaxID=143292;
RP [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319; DOI=10.1038/35054550;
RA O'Brien S.J.; Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals.";
DR EMBL; AY011374; AAG47409.1; -.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1547 MW; 5D6B97CA2D19C9C3 CRC64;

Query Match 26.6%; Score 25; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NPVHFFPKNI 11
Db 1 NPTYKFFEQM 10

RESULT 12
Q9BFR5 PRELIMINARY; PRT; 12 AA.
AC Q9BFR5;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
GN Amyloid beta protein (Fragment).
OS Name=APP;
OC Ursus arctos (Brown bear) (Grizzli bear).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
RN NCBI_TaxID=9644;
RP [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319; DOI=10.1038/35054550;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals.";
DR EMBL; AY011373; AAG47408.1; -.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1547 MW; 5D6B97CA2D19C9C3 CRC64;

Query Match 26.6%; Score 25; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NPVHFFPKNI 11
Db 1 NPTYKFFEQM 10

RESULT 13
Q9BFR6 PRELIMINARY; PRT; 12 AA.
```

```
AC Q9BFR6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
GN Amyloid beta protein (Fragment).
OS Name=APP;
OC Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN NCBI_TaxID=9615;
RP [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319; DOI=10.1038/35054550;
RA O'Brien S.J.; Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals.";
DR EMBL; AY011372; AAG47407.1; -.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1547 MW; 5D6B97CA2D19C9C3 CRC64;

Query Match 26.6%; Score 25; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NPVHFFPKNI 11
Db 1 NPTYKFFEQM 10

RESULT 14
Q9BFR7 PRELIMINARY; PRT; 12 AA.
AC Q9BFR7;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
GN Amyloid beta protein (Fragment).
OS Name=APP;
OC Panthera onca (Jaguar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Panthera.
RN NCBI_TaxID=9690;
RP [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319; DOI=10.1038/35054550;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals.";
DR EMBL; AY011371; AAG47406.1; -.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1547 MW; 5D6B97CA2D19C9C3 CRC64;

Query Match 26.6%; Score 25; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NPVHFFPKNI 11
Db 1 NPTYKFFEQM 10

RESULT 15
Q9BFR8 PRELIMINARY; PRT; 12 AA.
AC Q9BFR8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
GN Name=APP;
OC Leopardus pardalis (Ocelot).
```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Leopardus.  
OX NCB1\_TaxID=32538;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21082082; PubMed=11214319; DOI=10.1038/35054550;  
RA Murphy W.U., Bizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
O'Brien S.U.;  
RT "Molecular phylogenetics and the origins of placental mammals.";  
RL Nature 409:614-618(2001).  
DR EMBL; AY011370; AAC47405.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 12 AA; 1547 MW; 5D6B97CA2D19C9C3 CRC64;  
QY 2 NPVHFFKNI 11  
|||:  
Db 1 NPTYKFFEQM 10

Search completed: June 7, 2005, 09:36:30  
UOD time : 166 secs

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OM protein - protein search, using sw model

Run on: June 7, 2005, 09:33:36 ; Search time 67 Seconds  
(without alignments)  
98.133 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94  
Sequence: 1 ENPVVHFKNIVTPRTP 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 664154

Minimum DB seq length: 0  
Maximum DB seq length: 17

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1908:.\*  
2: geneseqp1908:.\*  
3: geneseqp2000:.\*  
4: geneseqp2001:.\*  
5: geneseqp2002:.\*  
6: geneseqp2003:.\*  
7: geneseqp2003:.\*  
8: geneseqp2004:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	100.0	17	3	AAV69395
2	94	100.0	17	5	AAO20308
3	94	100.0	17	5	AAE26359
4	94	100.0	17	5	AAE23935
5	94	100.0	17	6	ABP97941
6	94	100.0	17	6	ABRS6063
7	94	100.0	17	6	AAO19672
8	94	100.0	17	7	ADBS0773
9	94	100.0	17	8	ADK67704
10	94	100.0	17	8	ADL18291
11	89	94.7	17	2	AAK44116
12	89	94.7	17	2	AAW35360
13	89	94.7	17	2	AAW3601
14	89	94.7	17	3	AAV66534
15	87	92.6	17	2	AAK44118
16	87	92.6	17	2	AAW35354
17	87	92.6	17	2	AAW72353
18	87	92.6	17	2	AAW73602
19	83	88.3	16	2	AAK44117
20	83	88.3	16	2	AAW35361
21	83	88.3	16	3	AAV66535
22	83	88.3	16	5	AAE23936
23	82	87.2	15	2	AAK44120
24	82	87.2	15	2	AAW05498
25	82	87.2	15	2	AAW04856

26	82	87.2	15	2	AAW78826	AAW78826	Myelin ba
27	82	87.2	15	2	AAW73599	AAW73599	Human mye
28	82	87.2	15	3	AAV85545	AAV85545	Human MBP
29	82	87.2	15	3	AAW85528	AAW85528	Human MBP
30	82	87.2	15	3	AAW33638	AAW33638	MHC class
31	82	87.2	15	3	AAW12630	AAW12630	Human mye
32	82	87.2	15	4	AAW99039	AAW99039	Vaccine T
33	82	87.2	15	4	AAW93734	AAW93734	Human mye
34	82	87.2	15	5	AAO20312	AAO20312	Myelin ba
35	82	87.2	15	5	AAO17039	AAO17039	Myelin ba
36	82	87.2	15	5	ABP52207	ABP52207	Myelin ba
37	82	87.2	15	5	ABW84358	ABW84358	Human BPI
38	82	87.2	15	6	AAE33459	AAE33459	MBP85-99
39	82	87.2	15	6	ABR44413	ABR44413	Human bas
40	82	87.2	15	6	ABR44414	ABR44414	Human bas
41	82	87.2	15	6	ABU96590	ABU96590	MHC class
42	82	87.2	15	7	ADW89023	ADW89023	Ordered p
43	82	87.2	15	7	ADC06708	ADC06708	MBP p85-9
44	82	87.2	15	7	ADW38272	ADW38272	Immunomod
45	82	87.2	15	8	AD129030	AD129030	MBP (85-9

#### ALIGNMENTS

RESULT 1	
AAV69395	
ID	AAV69395 standard; peptide; 17 AA.
XX	
XX	AAV69395;
DT	
XX	19-JUN-2000 (first entry)
DE	
XX	Peptide derived from a human myelin basic protein.
XX	
XX	Human; myelin basic protein; oligodendroglial cell; Th2 immune response;
KW	Th2-type cytokine; analogue; multiple sclerosis.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
PN	WO200011027-A1.
XX	
PD	02-MAR-2000.
XX	
PF	19-AUG-1999; 99WO-US019033.
XX	
PR	20-AUG-1998; 98US-00137759.
XX	
PA	(NOVS ) NOVARTIS AG.
PA	(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PA	(NEUR-) NEUROCRINE BIOSCIENCES INC.
PI	
PI	Gaur A, Conlon P, Ling NC, Staehlin T, Crowe P;
DR	WPI; 2000-224661/19.
PT	
PT	Inducing a Th2 immune response and a persistent systemic immune response
PT	to myelin basic protein, MBP, or a peptide analog of MBP for use in
PT	treating multiple sclerosis, by administering compositions comprising
PT	peptide analogs of MBP.
XX	
PS	Example 10; Fig 8; 112pp; English.
XX	
CC	The present sequence represents a peptide derived from human myelin basic
CC	protein. Myelin basic protein is found in the cytoplasm of human
CC	oligodendroglial cells. Peptide analogue derived from the present
CC	sequence are administered to a patient in need to induce a Th2 immune
CC	response (i.e. production of T cells producing one or more Th2-type
CC	cytokines) and/or a persistent systemic immune response to myelin basic
CC	protein. These peptide analogues are at least seven amino acids long,
CC	derived from residues 83-99 of human myelin basic protein and altered
CC	from the native sequence at least at positions 91, 95 or 97. The peptide

CC analogs are especially useful in the treatment of multiple sclerosis  
XX  
SQ Sequence 17 AA;  
Query Match 100.0%; Score 94; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
DB 1 ENPVVHFFKNIVTPRTP 17  
RESULT 2  
AAO20308  
ID AAO20308 standard; peptide; 17 AA.  
AC AAO20308;  
XX  
DT 31-MAY-2002 (first entry)  
XX  
DE Myelin basic protein (MBP) aptope peptide region 83-99.  
XX  
KM MBP; myelin basic protein; aptope; antiasthmatic; tolerogenic peptide;  
dermatological; antiinflammatory; neuroprotective; antidiabetic; antianemic;  
vasotropic; antihistaminic; immunosuppressive; antidiabetic; class I;  
major histocompatibility complex; MHC; class II; autoimmune thyroiditis;  
hypersensitivity disorder; antigen; allergy; extrinsic asthma; urticaria;  
autoimmune haemolytic anaemia; atopic dermatitis; allergic rhinitis;  
autoimmune disease; multiple sclerosis; Grave's disease; sarcoidosis;  
systemic sclerosis; polymyositis; diabetes; transplant rejection;  
antiviral CD8+.  
XX  
OS Unidentified.  
XX  
PN WO200216410-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 17-AUG-2001; 2001WO-GB003702.  
XX  
PR 21-AUG-2000; 2000GB-00020618.  
PR 14-JUN-2001; 2001GB-00014547.  
XX  
(UYBR-) UNITV BRISTOL.  
XX  
PI Wraith DC, Anderton SM, Maza G, Ponsford M, Streeter HB;  
XX  
DR MPI; 2002-292056/33.  
XX  
PT Selecting tolerogenic peptide useful for treating autoimmune diseases  
e.g. multiple sclerosis, involves selecting peptide which binds major  
histocompatibility complex class I or II molecule without further  
processing.  
XX  
PS Claim 12; Page 28; 55pp; English.  
XX  
CC The invention relates to a method for selecting a tolerogenic peptide,  
comprising selecting a peptide which is capable of binding to a major  
histocompatibility complex (MHC) class I or II molecule without further  
processing. The peptides of the invention are useful for preventing a  
disease such as hypersensitivity disorder, and also for treating and/or  
preventing a disease in a subject. The method involves identifying an  
antigen for the disease, identifying an aptope (antigen processing  
independent epitope) for the antigen, and administering the aptope to  
the subject. The peptides of the invention are also useful for treating  
allergies such as extrinsic asthma, atopic dermatitis, allergic rhinitis,  
urticaria, autoimmune diseases such as multiple sclerosis, autoimmune  
thyroiditis, Grave's disease, systemic sclerosis, sarcoidosis, autoimmune  
haemolytic anaemia, polymyositis, diabetes, etc., and transplant  
rejection. The peptides are also useful for modifying antiviral CD8+  
responses in a tolerogenic fashion. This sequence represents an aptope  
of the invention of peptide region 83-99 of Myelin basic protein (MBP)

XX  
SQ Sequence 17 AA;  
Query Match 100.0%; Score 94; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
DB 1 ENPVVHFFKNIVTPRTP 17  
RESULT 3  
AAE26359  
ID AAE26359 standard; peptide; 17 AA.  
AC AAE26359;  
XX  
DT 13-DEC-2002 (first entry)  
XX  
DE Peptide related to myelin basic protein.  
XX  
KM Th2 immune response; myelin basic protein; MBP; vaccine; MS;  
multiple sclerosis; antisclerotic.  
XX  
OS Unidentified.  
XX  
PN US6379670-B1.  
XX  
PD 30-APR-2002.  
XX  
PF 19-AUG-1999; 99US-00378244.  
PR 18-NOV-1994; 94US-00342408.  
PR 20-AUG-1998; 98US-00137759.  
XX  
PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
PA (NOVS) NOVARTIS AG.  
XX  
PI Gaur A, Conlon P, Ling NC, Staehelin T, Crowe PD;  
XX  
DR MPI; 2002-461895/49.  
XX  
PT Inducing Th2 immune responses to Myelin Basic Protein (MBP) by  
administering the MBP peptide analog CGP 77116, useful for treating  
Multiple Sclerosis.  
XX  
PS Disclosure; Col 35-36; 49pp; English.  
XX  
CC The present invention relates to a novel method for inducing Th2 immune  
responses to Myelin Basic Protein (MBP) or a peptide analogue of MBP in a  
patient. The method involves administering a composition comprising the  
MBP peptide analogue CGP 77116 (NBI-5788). The method is useful for  
treating multiple sclerosis (MS). Sequences of the invention are also  
used as vaccines. The present sequence is a peptide related to human MBP  
XX  
SQ Sequence 17 AA;  
Query Match 100.0%; Score 94; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
DB 1 ENPVVHFFKNIVTPRTP 17  
RESULT 4  
AAE23935  
ID AAE23935 standard; peptide; 17 AA.  
XX  
AC AAE23935;  
XX



DT 10-SEP-2002 (first entry)  
XX Peptide analogue used in the invention.  
DE Autoimmune disease; multiple sclerosis; MS; Jbeta; Cbeta; Vbeta; Dbeta;  
XX immunosuppressive; T-cell receptor; therapy.  
XX Unidentified.  
XX WO200216434-A1.  
XX 28-FEB-2002.  
XX  
XX 22-AUG-2000; 2000WO-US022988.  
XX 22-AUG-2000; 2000WO-US022988.  
XX (BAYU ) BAYLOR COLLEGE MEDICINE.  
XX Zhang JZ;  
XX WPI; 2002-454317/48.  
XX A novel peptide used in the treatment of autoimmune disease e.g. multiple  
XX sclerosis.  
XX  
XX Example 2; Fig 2; 64pp; English.  
XX  
XX The invention relates to a peptide used in the treatment of autoimmune  
XX disease e.g. multiple sclerosis (MS). More particularly, it concerns a T-  
XX cell receptor sequence found in some MS patients and methods for its  
XX detection. T cell receptors comprise alpha and beta chains, with beta  
XX chains comprising the following regions from N-terminus to C-terminus:  
XX Vbeta-Dbeta-Dbeta-Cbeta. T cell receptors naturally vary in the Vbeta-  
XX Dbeta-beta region. The peptides of the invention are used for treating  
XX autoimmune disease e.g multiple sclerosis. The present sequence is a  
XX peptide analogue used in the exemplification of the invention  
XX  
XX Sequence 17 AA:  
SQ  
Query Match 100.0%; Score 94; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
DB 1 ENPVVHFFKNIVTPRTP 17  
RESULT 5  
ABP97941  
ID ABP97941 standard; peptide; 17 AA.  
XX  
XX ABP97941;  
XX  
XX 17-JUN-2003 (first entry)  
XX  
XX Amino acid sequence of a glycopeptide.  
XX  
XX Glycopeptide; serum; immunosorption column; antibody;  
XX multiple sclerosis.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
XX Modified-site 1 /note= "H attached"  
XX Modified-site 2 /note= "glycosylated residue"  
XX Modified-site 17 /note= "OH attached"  
XX  
XX WO2003009887-A2.

XX  
XX 06-FEB-2003.  
XX  
XX 25-JUL-2002; 2002WO-EP008274.  
XX  
XX 25-JUL-2001; 2001IT-FI000144.  
XX  
XX (UYFI-) UNIV FIRENZE.  
XX  
XX Pinto F, Papini AM, Chelli M, Rovero P, Lolli F;  
XX  
XX WPI; 2003-312632/30.  
XX  
XX Immunosorption column, useful for treating multiple sclerosis, contains  
XX glycopeptides able to react with disease-specific autoantibodies.  
XX  
XX Claim 4; Page 6; 13pp; English.  
XX  
XX ABP97937-44 represent glycopeptides of a formula given in the  
XX CC specification. The glycopeptides are used to produce columns of the  
XX CC invention. The specification describes immunosorption columns,  
XX CC containing conjugates comprising glycopeptides which are able to  
XX CC recognize antibodies implicated in multiple sclerosis. The column removes  
XX CC harmful antibodies selectively, leaving all other components of the serum  
XX CC unchanged. The column is used to treat multiple sclerosis  
XX  
XX Sequence 17 AA:  
SQ  
Query Match 100.0%; Score 94; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
DB 1 ENPVVHFFKNIVTPRTP 17  
RESULT 6  
ABR56063  
ID ABR56063 standard; peptide; 17 AA.  
XX  
XX ABR56063;  
XX  
XX 06-AUG-2003 (first entry)  
XX  
XX Glycopeptide #5 for diagnosis and treatment of multiple sclerosis.  
XX  
XX Glycopeptide; neuroprotective; autoantibody; multiple sclerosis.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
XX Modified-site 2 /note= "Asn(Glc)"  
XX  
XX WO2003000733-A2.  
XX  
XX 03-JAN-2003.  
XX  
XX 19-JUN-2002; 2002WO-EP006767.  
XX  
XX 22-JUN-2001; 2001IT-FI000114.  
XX  
XX (UYFI-) UNIV FIRENZE.  
XX  
XX Papini AM, Chelli M, Rovero P, Lolli F;  
XX  
XX WPI; 2003-354383/33.  
XX  
XX Novel glycopeptides comprising a specific tetrapeptide, useful as  
XX diagnostic tools for identifying multiple sclerosis.  
XX  
XX Claim 7; Page 12; 14pp; English.

XX The present invention relates to glycopeptides (ABR56059-ABR56066). The  
CC glycopeptides have high specificity in recognizing autoantibodies  
CC involved in multiple sclerosis pathology, and thus are effectively used  
CC in diagnosis and treatment for multiple sclerosis  
XX  
SQ Sequence 17 AA:  
Query Match 100.0%; Score 94; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6,1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
1 |||||||||||||  
Db 1 ENPVVHFFKNIVTPRTP 17  
RESULT 7  
ID AAO19672 standard; peptide; 17 AA.  
XX AAO19672;  
XX  
XX 28-MAR-2003 (first entry)  
XX  
XX Human myelin basic protein MBP minimal epitope.  
XX  
XX Human; Ig; immunoglobulin; immunotherapy; immune disease; MBP;  
XX Fcpepsilon receptor; autoimmune disease; constant region; heavy chain;  
XX antiasthmatic; antiallergic; antiinflammatory; dermatological; GS2;  
XX antischistosomal; antineoplastic; antidiabetic; neuroprotective;  
XX myelin basic protein; minimal epitope.  
XX  
XX Homo sapiens.  
XX  
XX WO200288317-A2.  
XX  
XX 07-NOV-2002.  
XX  
XX 01-MAY-2002; 2002WO-US013527.  
XX  
XX 01-MAY-2001; 2001US-00847208.  
XX  
XX 24-OCT-2001; 2001US-00000439.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Saxon A, Zhang K, Zhu D;  
XX  
XX MPI; 2003-103456/09.  
XX  
XX New fusion molecules comprising polypeptide sequences that bind to IgG  
XX inhibitory receptor and native IgE receptor, useful for treating IgE-  
XX mediated hypersensitivity reactions, e.g. asthma or allergies, or  
XX autoimmune diseases.  
XX  
XX Claim 23; Page 116; 116pp; English.  
XX  
XX The present invention relates to a fusion molecule comprising a first  
XX polypeptide sequence capable of specific binding to a native IgG  
XX inhibitory receptor consisting of an immune receptor tyrosine-based  
XX inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,  
XX functionally connected to a second polypeptide sequence capable of  
XX specific binding directly or indirectly to a native IgE receptor  
XX (Fcpepsilon). Also provided are nucleotide sequences encoding such a  
XX fusion protein. The fusion molecules and compositions are useful for  
XX treating an IGE-mediated biological response, preferably an IGE-mediated  
XX hypersensitivity reaction, such as asthma, allergic rhinitis, atopic  
XX dermatitis, severe food allergies, chronic urticaria, angioedema or  
XX anaphylactic shock; or autoimmune diseases such as Rheumatoid arthritis,  
XX type-I diabetes mellitus, or multiple sclerosis, and for preventing of,  
XX or symptoms resulting from, a type I hypersensitivity reaction in a  
XX subject receiving immunotherapy. The present sequence is the human myelin  
XX basic protein minimal epitope which can be used in a fusion protein of

CC the invention  
XX  
XX Sequence 17 AA:  
SQ  
Query Match 100.0%; Score 94; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6,1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
1 |||||||||||||  
Db 1 ENPVVHFFKNIVTPRTP 17  
RESULT 8  
ID ADE50773 standard; peptide; 17 AA.  
XX ADE50773;  
XX  
XX 29-JAN-2004 (first entry)  
XX  
XX Wild-type human myelin basic protein peptide analog.  
XX  
XX Human; Th2; immune response; myelin basic protein; peptide analog;  
XX proteolysis; multiple sclerosis; neuroprotective; gene therapy.  
XX  
XX Homo sapiens.  
XX  
XX US2002176866-A1.  
XX  
XX 28-NOV-2002.  
XX  
XX 20-MAR-2002; 2002US-00104973.  
XX  
XX 18-NOV-1994; 94US-00342408.  
XX  
XX 20-AUG-1998; 98US-00137759.  
XX  
XX 19-AUG-1999; 99US-00378244.  
XX  
XX (NEUR-) NEUROCRINE BIOSCIENCES INC.  
XX  
XX Gaur A, Conlon P, Ling NC, Staehelin T, Crowe PD;  
XX  
XX MPI; 2003-615722/58.  
XX  
XX Disclosure, SEQ ID NO 3; 52pp; English.  
XX  
XX The invention discloses a method for inducing a Th2 immune response to  
XX myelin basic protein or its peptide analog in a patient, comprising  
XX administering a composition comprising a peptide analog in combination  
XX with a carrier/adjuvant or diluent. The peptide analog comprises at least  
XX 7 amino acids selected from residues 83 to 99 of human myelin basic  
XX protein, where: the L-lysine at position 91, L-arginine at position 97 or  
XX L-threonine at position 95, is altered to another amino acid, and one to  
XX three L-amino acids selected from valine at position 86 or 87, histidine  
XX at position 88, threonine at position 95 or 98, and proline at position  
XX 99 are altered to an amino acid other than the amino acid present in the  
XX native protein at that position or the L-lysine at position 91 is altered  
XX to another amino acid and the N- and/or C-terminal amino acid are altered  
XX to another amino acid, such that upon administration of the peptide  
XX analog in vivo proteolysis is reduced. The peptide analog comprises 7-17  
XX amino acids and one to four additional altered residues. The N-terminal  
XX amino acid is residue 83 of human myelin basic protein. At least one of  
XX the additional L-amino acids selected from residues 83 to 90 and 92 to 99  
XX is substituted with a charged amino acid. The method is useful for  
XX treating multiple sclerosis using peptide analogs of human myelin basic  
XX protein. The sequence presented is the wild-type human myelin basic  
XX protein peptide analog.

TYPE: PRT  
ORGANISM: synthetic construct  
US-09-836-433-30

Query Match 100.0%; Score 94; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.5e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
|||||  
3 ENPVVHFFKNIVTPRTP 19

RESULT 13

US-09-859-012-35  
Sequence 35, Application US/09859012  
Publication No. US20040253632A1

GENERAL INFORMATION:

APPLICANT: RHODE, PETER

APPLICANT: WITTMAN, VAUGHAN

APPLICANT: WEIDMANZ, JON A.

APPLICANT: BURKHARDT, MARTIN

APPLICANT: CARD, KIMBERLYN F.

APPLICANT: TAL, RONY

APPLICANT: ACEVEDO, JORGE

APPLICANT: WONG, HING C.

TITLE OF INVENTION: MODULATION OF T CELL RECEPTOR INTERACTIONS

FILE REFERENCE: 49444 (71758)

CURRENT APPLICATION NUMBER: US/09/859,012

PRIOR FILING DATE: 2001-05-16

PRIOR APPLICATION NUMBER: 60/206,920

NUMBER OF SEQ ID NOS: 49

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 35

LENGTH: 20

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-859-012-35

Query Match 100.0%; Score 94; DB 11; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.5e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
|||||  
3 ENPVVHFFKNIVTPRTP 19

RESULT 14

US-09-859-012-49  
Sequence 49, Application US/09859012  
Publication No. US20040253632A1

GENERAL INFORMATION:

APPLICANT: RHODE, PETER

APPLICANT: WITTMAN, VAUGHAN

APPLICANT: WEIDMANZ, JON A.

APPLICANT: BURKHARDT, MARTIN

APPLICANT: CARD, KIMBERLYN F.

APPLICANT: TAL, RONY

APPLICANT: ACEVEDO, JORGE

APPLICANT: WONG, HING C.

TITLE OF INVENTION: MODULATION OF T CELL RECEPTOR INTERACTIONS

FILE REFERENCE: 49444 (71758)

CURRENT APPLICATION NUMBER: US/09/859,012

PRIOR FILING DATE: 2001-05-16

PRIOR APPLICATION NUMBER: 60/206,920

NUMBER OF SEQ ID NOS: 49

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 49  
LENGTH: 20  
TYPE: PRT

ORGANISM: Homo sapiens  
US-09-859-012-49

Query Match 100.0%; Score 94; DB 11; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.5e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
|||||  
3 ENPVVHFFKNIVTPRTP 19

RESULT 15

US-10-081-281-33

Sequence 33, Application US/10081281  
Publication No. US20020151707A1

GENERAL INFORMATION:

APPLICANT: Kindsvogel, Wayne

Gross, Jane A.

Sheppard, Paul

TITLE OF INVENTION: Immune Mediators and Related Methods

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/081,281

FILING DATE: 20-Feb-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/261,811A

FILING DATE: 03-Mar-1999

APPLICATION NUMBER: US 08/480,002

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/482,133

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/483,241

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 60/005,964

FILING DATE: 27-OCT-1995

APPLICATION NUMBER: US 08/657,581

FILING DATE: 07-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Parent, Annette S.

REGISTRATION NUMBER: 42,058

REFERENCE/DOCKET NUMBER: 014058-005630US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 33:

US-10-081-281-33

Query Match 100.0%; Score 94; DB 13; Length 21;  
Best Local Similarity 100.0%; Pred. No. 5.8e-08;

Matches	17;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	ENPVVHFFKNIVTPRTP	17						
Db	2	ENPVVHFFKNIVTPRTP	18						

Search completed: June 7, 2005, 09:25:08  
Job time : 8.45769 secs

GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: June 7, 2005, 09:33:36 ; Search time 40 Seconds  
(without alignments)  
31.726 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94

Sequence: 1 ENPVVHFFKNIVTPRTP 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 segs, 74649064 residues

Total number of hits satisfying chosen parameters: 177072

Minimum DB seq length: 0  
Maximum DB seq length: 17  
Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/prodata/1/iaa/backfilltest.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	100.0	17	3	US-09-137-759-3
2	94	100.0	17	3	US-09-378-244-3
3	89	94.7	17	2	US-08-468-540B-19
4	87	92.6	17	2	US-08-468-540B-20
5	82	87.2	15	1	US-08-787-547-37
6	82	87.2	15	2	US-08-468-540B-16
7	82	87.2	15	2	US-08-400-796-16
8	82	87.2	15	4	US-09-606-254-11
9	82	87.2	16	2	US-08-468-540B-21
10	81.9	81.9	14	2	US-08-468-540B-23
11	77	81.9	15	2	US-08-468-540B-22
12	76	80.9	14	3	US-08-342-408B-3
13	76	80.9	16	4	US-09-009-953-3
14	75	79.8	17	3	US-09-137-759-6
15	75	79.8	17	3	US-09-378-244-6
16	72	76.6	13	2	US-08-540-388-4
17	72	76.6	13	2	US-08-735-253-19
18	71	75.5	17	3	US-09-137-759-7
19	71	75.5	17	3	US-09-378-244-7
20	70	74.5	14	1	US-08-787-547-36
21	69	73.4	17	3	US-09-137-759-8
22	69	73.4	17	3	US-09-378-244-8
23	68	72.3	13	1	US-08-787-547-38
24	68	72.3	13	5	PCT-US94-10257A-22
25	68	72.3	13	5	PCT-US94-10257A-24
26	66	70.2	17	3	US-09-137-759-5
27	66	70.2	17	3	US-09-378-244-5

28	64	68.1	17	3	US-09-137-759-4	Sequence 4, Appl1
29	64	68.1	17	3	US-09-378-244-4	Sequence 4, Appl1
30	60	63.8	12	4	US-09-403-752A-126	Sequence 126, App
31	60	63.8	12	4	US-09-551-151A-126	Sequence 126, App
32	57	60.6	13	1	US-08-483-021-4	Sequence 9, Appl1
33	56	59.6	10	3	US-08-159-339A-1097	Sequence 1097, Ap
34	56	59.6	10	3	US-08-159-339A-1109	Sequence 1109, Ap
35	53	56.4	14	3	US-08-855-925A-6	Sequence 6, Appl1
36	52	55.3	10	4	US-09-606-254-9	Sequence 9, Appl1
37	48	51.1	12	3	US-08-462-351-9	Sequence 9, Appl1
38	48	51.1	12	4	US-09-602-807-9	Sequence 9, Appl1
39	34	36.2	15	2	US-08-400-796-11	Sequence 11, Appl1
40	33	35.1	9	2	US-08-340-283-13	Sequence 13, Appl1
41	30	31.9	10	3	US-08-159-339A-461	Sequence 461, App
42	30	31.9	14	3	US-09-313-677-3	Sequence 3, Appl1
43	30	31.9	16	4	US-08-077-797A-49	Sequence 49, Appl1
44	30	31.9	16	4	US-09-546-013-78	Sequence 78, Appl1
45	30	31.9	16	5	PCT-US94-01238-49	Sequence 49, Appl1

## ALIGNMENTS

```

RESULT 1
; US-09-137-759-3
; Sequence 3, Application US/09137759
; Patent No. 6251396
; GENERAL INFORMATION:
; APPLICANT: Gaur, Amitabh
; APPLICANT: Conlon, Paul J.
; APPLICANT: Ling, Nicholas C.
; APPLICANT: Staehlin, Theophil
; APPLICANT: Crowe, Paul D.
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING
; TITLE OF INVENTION: PEPTIDE ANALOGS OF HUMAN MYELIN BASIC PROTEIN
; FILE REFERENCE: 690068.405C1
; CURRENT APPLICATION NUMBER: US/09/137,759
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; US-09-137-759-3

Query Match      100.0%; Score 94; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ENPVVHFFKNIVTPRTP 17
Db      1 ENPVVHFFKNIVTPRTP 17

RESULT 2
; US-09-378-244-3
; Sequence 3, Application US/09378244
; Patent No. 6379670
; GENERAL INFORMATION:
; APPLICANT: Gaur, Amitabh
; APPLICANT: Conlon, Paul J.
; APPLICANT: Ling, Nicholas C.
; APPLICANT: Staehlin, Theophil
; APPLICANT: Crowe, Paul D.
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING
; TITLE OF INVENTION: PEPTIDE ANALOGS OF HUMAN MYELIN BASIC PROTEIN
; FILE REFERENCE: 690068.405C2
; CURRENT APPLICATION NUMBER: US/09/378,244
; CURRENT FILING DATE: 1999-08-19

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; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis
US-09-378-244-3

Query Match      100.0%; Score 94; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ENPVVHFFKNIVTPRT 17
        |||
Db      1 ENPVVHFFKNIVTPRT 17

RESULT 3
US-08-468-540B-19
; Sequence 19, Application US/08468540B
; Patent No. 5858980
; GENERAL INFORMATION:
; APPLICANT: Weiner, Howard
; APPLICANT: Hafner, David
; APPLICANT: Miller, Ariel
; APPLICANT: Al-Sabbagh, Ahmad
; TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
; TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,540B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jacobs, Seth H
; REGISTRATION NUMBER: 32,140
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: NO. 5858980e
US-08-468-540B-19

Query Match      94.7%; Score 89; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 NEVVFHFFKNIVTPRT 17
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```

Db      1 NEVVFHFFKNIVTPRT 16

RESULT 4
US-08-468-540B-20
; Sequence 20, Application US/08468540B
; Patent No. 5858980
; GENERAL INFORMATION:
; APPLICANT: Weiner, Howard
; APPLICANT: Hafner, David
; APPLICANT: Miller, Ariel
; APPLICANT: Al-Sabbagh, Ahmad
; TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
; TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,540B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jacobs, Seth H
; REGISTRATION NUMBER: 32,140
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: NO. 5858980e
US-08-468-540B-20

Query Match      92.6%; Score 87; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.8e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ENPVVHFFKNIVTPRT 16
        |||
Db      2 ENPVVHFFKNIVTPRT 17

RESULT 5
US-08-787-547-37
; Sequence 37, Application US/08787547
; Patent No. 5783567
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Curley, Joanne M.
; APPLICANT: Langer, Robert S.
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
; TITLE OF INVENTION: OF NUCLEIC ACID
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/787,547  
FILING DATE: 22-JAN-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 08191/003001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-787-547-37

Query Match 87.2%; Score 82; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. Se-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVHFFKNIVTPR 15  
Db 1 ENPVHFFKNIVTPR 15

RESULT 6  
US-08-468-540B-16  
Sequence 16, Application US/08468540B  
Patent No. 5858980  
GENERAL INFORMATION:  
APPLICANT: Weiner, Howard  
APPLICANT: Hafner, David  
APPLICANT: Miller, Ariel  
APPLICANT: Al-Sabbagh, Ahmad  
TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION  
TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Darby & Darby P.C.  
STREET: 805 Third Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,540B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jacobs, Seth H  
REGISTRATION NUMBER: 32,140  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 5858980e  
US-08-468-540B-16

Query Match 87.2%; Score 82; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. Se-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVHFFKNIVTPR 15  
Db 1 ENPVHFFKNIVTPR 15

RESULT 7  
US-08-400-796-16  
Sequence 16, Application US/08400796  
Patent No. 5874531  
GENERAL INFORMATION:  
APPLICANT: STROMINGER, JACK L.  
APPLICANT: MICHERPENNING, KAI  
TITLE OF INVENTION: IDENTIFICATION OF SELF AND NON-SELF  
TITLE OF INVENTION: ANTIGENS IMPLICATED IN AUTOIMMUNE DISEASE  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
STREET: 600 ATLANTIC AVENUE  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/400,796  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: TWOMEY, MICHAEL J.  
REGISTRATION NUMBER: 38,349  
REFERENCE/DOCKET NUMBER: H0498/7015  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: Internal  
ORIGINAL SOURCE:  
ORGANISM: HOMO SAPIENS  
US-08-400-796-16

Query Match 87.2%; Score 82; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 5e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPR 15  
| | | | | | | | | |  
DB 1 ENPVVHFFKNIVTPR 15

## RESULT 8

US-09-606-254-11  
; Sequence 11, Application US/09606254  
; Patent No. 6531130  
; GENERAL INFORMATION:  
; APPLICANT: Steinman, Lawrence  
; APPLICANT: Ruiz, Pedro  
; TITLE OF INVENTION: Treatment of Demyelinating Autoimmune  
; TITLE OF INVENTION: Disease with Ordered Peptides  
; FILE REFERENCE: STAN-129  
; CURRENT APPLICATION NUMBER: US/09/606,254  
; CURRENT FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/142,479  
; PRIOR FILING DATE: 1999-07-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
US-09-606-254-11

Query Match 87.2%; Score 82; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPR 15  
| | | | | | | | | |  
DB 1 ENPVVHFFKNIVTPR 15

## RESULT 9

US-08-468-540B-21  
; Sequence 21, Application US/08468540B  
; Patent No. 5858980  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, Howard  
; APPLICANT: Hafler, David  
; APPLICANT: Miller, Ariel  
; APPLICANT: Al-Sabbagh, Ahmad  
; TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION  
; TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Darby & Darby P.C.  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10022

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,540B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:

NAME: Jacobs, Seth H  
REGISTRATION NUMBER: 32,140  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX:

INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 5858980e  
US-08-468-540B-21

Query Match 87.2%; Score 82; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPR 15  
| | | | | | | | | |  
DB 2 ENPVVHFFKNIVTPR 16

## RESULT 10

US-08-468-540B-23  
; Sequence 23, Application US/08468540B  
; Patent No. 5858980  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, Howard  
; APPLICANT: Hafler, David  
; APPLICANT: Miller, Ariel  
; APPLICANT: Al-Sabbagh, Ahmad  
; TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION  
; TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Darby & Darby P.C.  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10022

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,540B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jacobs, Seth H  
REGISTRATION NUMBER: 32,140  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX:

INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 5858980e  
US-08-468-540B-23



Query Match 81.9%; Score 77; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred.No.3.1e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2 NPVHFFKNIVTPR 15  
Db 1 NPVHFFKNIVTPR 14

RESULT 11  
US-08-468-540B-22  
; Sequence 22, Application US/08468540B  
; Patent No. 5858980  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, Howard  
; APPLICANT: Hatler, David  
; APPLICANT: Miller, Ariel  
; APPLICANT: Al-Sabbagh, Ahmad  
; TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION  
; TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Darby & Darby P.C.  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468,540B  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jacobs, Seth H  
; REGISTRATION NUMBER: 32,140  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-527-7700  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: NO. 5858980e  
US-08-468-540B-22

Query Match 81.9%; Score 77; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred.No.3.3e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 ENPVHFFKNIVTP 14  
Db 2 ENPVHFFKNIVTP 15

RESULT 12  
US-08-342-408B-3  
; Sequence 3, Application US/08342408B  
; Patent No. 6328499  
; GENERAL INFORMATION:  
; APPLICANT: Ling, Nicholas  
; APPLICANT: Gaur, Amitabh

APPLICANT: Conlon, Paul J.  
; APPLICANT: Seilman, Lawrence  
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE  
; TITLE OF INVENTION: SCLEROSIS USING PEPTIDE ANALOGUES OF HUMAN MYELIN BASIC  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/342,408B  
; FILING DATE: 18-NOV-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6329499tenburg, Carol  
; REGISTRATION NUMBER: 39,317  
; REFERENCE/DOCKET NUMBER: 690068.405  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-342-408B-3

Query Match 80.9%; Score 76; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred.No.4.5e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 4 VVHFFKNIVTPRP 17  
Db 1 VVHFFKNIVTPRP 14

RESULT 13  
US-09-009-953-3  
; Sequence 3, Application US/09009953  
; Patent No. 6413517  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; TITLE OF INVENTION: Identification of Broadly  
; NUMBER OF SEQUENCES: 274  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/009,953  
; FILING DATE: 21-Jan-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/036,713

FILING DATE: 23-JAN-1997  
APPLICATION NUMBER: US 60/037,432  
FILING DATE: 07-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 018623-011520US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-009-953-3

Query Match 80.9%; Score 76; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.2e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VVHFFKNIVTPRT 17  
|||||  
DB 1 VVHFFKNIVTPRT 14

RESULT 14  
US-09-137-759-6  
; Sequence 6, Application US/09137759  
; Patent No. 6251396  
; GENERAL INFORMATION:  
; APPLICANT: Gaur, Amitabh  
; APPLICANT: Conlon, Paul J.  
; APPLICANT: Ling, Nicholas C.  
; APPLICANT: Staehlin, Theophil  
; APPLICANT: Crowe, Paul D.  
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING  
; FILE REFERENCE: 690068.405C1  
; CURRENT APPLICATION NUMBER: US/09/137,759  
; CURRENT FILING DATE: 1998-08-20  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: Where Xaa is a D-alanine residue  
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase  
; OTHER INFORMATION: Synthesis  
US-09-137-759-6

Query Match 79.8%; Score 75; DB 3; Length 17;  
Best Local Similarity 87.5%; Pred. No. 8e-06;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NPVHAFNIVTPRT 17  
|||||  
DB 2 NPVHAFNIVTPRT 17

RESULT 15  
US-09-378-244-6  
; Sequence 6, Application US/09378244  
; Patent No. 6379670

GENERAL INFORMATION:  
; APPLICANT: Gaur, Amitabh  
; APPLICANT: Conlon, Paul J.  
; APPLICANT: Ling, Nicholas C.  
; APPLICANT: Staehlin, Theophil  
; APPLICANT: Crowe, Paul D.  
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING  
; FILE REFERENCE: 690068.405C2  
; CURRENT APPLICATION NUMBER: US/09/378,244  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: Where Xaa is a D-alanine residue  
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase  
; OTHER INFORMATION: Synthesis  
US-09-378-244-6

Query Match 79.8%; Score 75; DB 3; Length 17;  
Best Local Similarity 87.5%; Pred. No. 8e-06;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NPVHAFNIVTPRT 17  
|||||  
DB 2 NPVHAFNIVTPRT 17

Search completed: June 7, 2005, 09:39:12  
Job time : 41 secs



XX  
DR MPI: 1393-351657/44.  
XX

PT New peptide(s) derived from human myelin basic protein - used for  
PT suppressing auto-immune response, partic. in treating multiple sclerosis.  
XX

PS Claim 1; Page 29; 118pp; English.  
XX

CC The peptide represents residues 84-100 of human myelin basic protein  
CC (hMBP). The fragment comprises an immunodominant epitope of hMBP which  
CC was identified by overlapping 20-mer oligopeptide sequence analysis using  
CC T-cell line assays. The peptide can be used to stop proliferation of  
CC human T-cells specific for MBP or to elicit active suppression of such T-  
CC cells. They are also used partic. for the treatment of multiple  
CC sclerosis. The peptide is also useful for identifying CD4+ T-cells  
CC reactive with MBP. See also AAR44114-25. (Updated on 25-MAR-2003 to  
CC correct PN field.)  
XX

SQ Sequence 17 AA;

Query Match 92.6%; Score 87; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.7e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ENPVVHFFKNIVTPT 16  
|||  
Db 2 ENPVVHFFKNIVTPT 17

Search completed: June 7, 2005, 09:38:28  
Job time : 70 secs

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OM protein - protein search, using sw model

Run on: June 7, 2005, 08:38:56 ; Search time 8.63212 Seconds  
(without alignments)  
761.681 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94

Sequence: 1 ENPVVHFPEKNIPTPT 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1808:\*  
2: geneseqp1908:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	100.0	17	3 AAY69395	Aay69395 Peptide d
2	94	100.0	17	5 AAO20308	Aao20308 Myelin ba
3	94	100.0	17	5 AAE26359	Aae26359 Peptide r
4	94	100.0	17	5 AAE23935	Aae23935 Peptide a
5	94	100.0	17	6 ABR97941	Abp97941 Amino aci
6	94	100.0	17	6 ABR56063	Abri56063 Glycopept
7	94	100.0	17	6 AAO19672	Aao19672 Human mye
8	94	100.0	17	7 ADE50773	Ade50773 Wild-type
9	94	100.0	17	8 ADK67704	Adk67704 Human mye
10	94	100.0	17	8 ADL18291	Adl18291 Human mye
11	94	100.0	18	2 AAR44115	Aar44115 Human mye
12	94	100.0	18	2 AAR95357	Aar95357 Residues
13	94	100.0	18	2 AAW73600	Aaw73600 Human mye
14	94	100.0	18	3 AAY66533	Aay66533 Myelin ba
15	94	100.0	19	2 AAR32295	Aar32295 Sequence
16	94	100.0	19	2 AAR44114	Aar44114 Human mye
17	94	100.0	19	2 AAR44123	Aar44123 Human mye
18	94	100.0	19	2 AAR85132	Aar85132 Human MBP
19	94	100.0	19	2 AAW05719	Aaw05719 Residues
20	94	100.0	19	2 AAR95366	Aar95366 Residues
21	94	100.0	19	2 AAR95358	Aar95358 Residues
22	94	100.0	19	2 AAR95358	Aar95358 Residues
23	94	100.0	19	2 AAW34183	Aaw34183 Bc-MBP (84
24	94	100.0	19	2 AAW34180	Aaw34180 Residues
25	94	100.0	19	2 AAW18021	Aaw18021 Human BPP

26	94	100.0	19	2 AAW44071	Aaw44071 Human mye
27	94	100.0	19	2 AAW73607	Aaw73607 Human mye
28	94	100.0	19	2 AAW73616	Aaw73616 Human mye
29	94	100.0	19	3 AAY58992	Aay58992 Myelin ba
30	94	100.0	19	3 AAY85560	Aay85560 Human MBP
31	94	100.0	19	3 AAY85550	Aay85550 Human MBP
32	94	100.0	19	3 AAY66532	Aay66532 Myelin ba
33	94	100.0	19	3 AAY66543	Aay66543 Myelin ba
34	94	100.0	19	3 AAB12618	Aab12618 Human mye
35	94	100.0	19	3 AAB12613	Aab12613 Human mye
36	94	100.0	19	4 AAM99040	Aam99040 Vaccine r
37	94	100.0	19	4 AAB74440	Aab74440 Ovalbumin
38	94	100.0	19	4 AAG65171	Aag65171 Myelin ba
39	94	100.0	19	5 AAB31665	Abg31665 Myelin ba
40	94	100.0	20	2 AAR94618	Aar94618 Myelin ba
41	94	100.0	20	2 AAR95392	Aar95392 Residues
42	94	100.0	20	2 AAW34187	Aaw34187 Bc-MBP (83
43	94	100.0	20	2 AAW34188	Aaw34188 Bc-MBP (83
44	94	100.0	20	2 AAW34184	Aaw34184 Bc-MBP (83
45	94	100.0	20	2 AAW34185	Aaw34185 Bc-MBP (83

## ALIGNMENTS

RESULT 1  
AAY69395  
ID AAY69395 standard; peptide; 17 AA.  
AC AAY69395;  
XX  
XX  
DT 19-JUN-2000 (first entry)  
XX  
DE Peptide derived from a human myelin basic protein.  
XX  
XX Human; myelin basic protein; oligodendroglial cell; Th2 immune response;  
KW Th2-type cytokine; analogue; multiple sclerosis.  
XX  
XX Synthetic.  
OS Homo sapiens.  
XX  
XX WO200011027-A1.  
XX  
XX 02-MAR-2000.  
XX  
XX 19-AUG-1999; 99WO-US019033.  
XX  
XX 20-AUG-1998; 98US-00137759.  
XX  
XX (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERB GES MBH.  
PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
XX  
XX Gaur A, Conlon P, Ling NC, Staehlin T, Crowe P,  
WPI; 2000-224661/19.  
XX  
XX Inducing a Th2 immune response and a persistent systemic immune response  
PT to myelin basic protein, MBP, or a peptide analog of MBP for use in  
PT treating multiple sclerosis, by administering compositions comprising  
PT peptide analogs of MBP.  
XX  
XX Example 10; Fig 8; 112pp; English.  
XX  
XX The present sequence represents a peptide derived from human myelin basic  
CC protein. Myelin basic protein is found in the cytoplasm of human  
CC oligodendroglial cells. Peptide analogue derived from the present  
CC sequence are administered to a patient in need to induce a Th2 immune  
CC response (i.e. production of T cells producing one or more Th2-type  
CC cytokines) and/or a persistent systemic immune response to myelin basic  
CC protein. These peptide analogues are at least seven amino acids long,  
CC derived from residues 83-99 of human myelin basic protein and altered  
CC from the native sequence at least at positions 91, 95 or 97. The peptide

CC analogs are especially useful in the treatment of multiple sclerosis  
XX  
SQ Sequence 17 AA;

XX Sequence 17 AA;  
SQ

Query Match	100.0%	Score 94	DB 3	Length 17
Best Local Similarity	100.0%	Pred. No. 6	Le-09	
Matches 17	Conservative 0	Mismatches 0	Indels 0	Gaps 0

**Oy** 1 ENPVVHFFKNIIVTPRP 17  
| | | | |  
**Oz** 1 ENPVVHFFKNIIVTPRP 17  
| | | | |

RESULT 2  
AAO20308  
ID AAO20308 standard; peptide; 17 AA.

AA	
DT	31-MAY-2002 (first entry)
XX	
DE	Myelin basic protein (MBP) epitope peptide region 83-99.

KM MB1: myelin basic protein; apolipoprotein; antiaesthatic; colerogenic peptide;  
 KM dermatological; antiallergic; neuroprotective; antihypoid; antinaemic;  
 KM vasoactive; antiinflammatory; immunosuppressive; antidiabetic; class I;  
 KM major histocompatibility complex; MHC; class II; autoimmune thyroiditis;  
 KM hyperaesthetic disorder; antigen; allergy; extrinsic asthma; urticaria;  
 KM autoimmune haemolytic anaemia; atopic dermatitis; allergic rhinitis;  
 KM autoimmune disease; multiple sclerosis; Grave's disease; sarcoidosis;  
 KM systemic sclerosis; polymyositis; diabetes; transplant rejection;  
 KM antiviral C8b+.

OS Unidentified.

PN WO200216410-A2.

PD 28-FEB-2002

PF 17-AUG-2001; 2001WO-GB003702.

PR 21-AUG-2000; 2000GB-00020618.  
PR 14-JUN-2001; 2001GB-00014547.

PA (UYBR-) UNIV BRISTOL.

PI Wraith DC, Anderton SM, Mazza G, Ponsford M, Streeter HB;

DR WPI; 2002-292056/33.

PT Selecting tolerogenic peptide useful for treating autoimmune diseases  
PT e.g. multiple sclerosis, involves selecting peptide which binds major  
PT histocompatibility complex class I or II molecule without further  
PT processing.

PS Claim 12; Page 28; 55pp; English.

CC The invention relates to a method for selecting a tolerogenic peptide,  
CC comprising selecting a peptide which is capable of binding to a major  
CC histocompatibility complex (MHC) class I or II molecule without further  
CC processing. The peptides of the invention are useful for preventing a  
CC disease such as hypersensitivity disorder, and also for treating and/or  
CC preventing a disease in a subject. The method involves identifying an  
CC antigen for the disease, identifying an aptope (antigen processing  
CC independent epitope) for the antigen, and administering the aptope to  
CC the subject. The peptides of the invention are also useful for treating  
CC allergies such as extrinsic asthma, atopic dermatitis, allergic rhinitis,  
CC urticaria, autoimmune diseases such as multiple sclerosis, autoimmune  
CC thyroiditis, Grave's disease, systemic sclerosis, sarcoidosis, autoimmune  
CC hemolytic anemia, polymyositis, diabetes, etc., and transplant  
CC rejection. The peptides are also useful for modifying antiviral CD8+  
CC responses in a tolerogenic fashion. This sequence represents an aptope  
CC of the invention of peptide region 83-99 of Myelin basic protein (MBP)

XX Sequence 17 AA;  
SQ

Query Match	100.0%	Score 94;	DB 5;	Length 17;
Best Local Similarity	100.0%	Pred. No. 6.1e-09;		
Matches 17; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

<b>QY</b>	<b>1</b>	ENPVVHFFKNIVTRTP	<b>17</b>
<b>Db</b>	<b>1</b>	ENPVVHFFKNIVTRTP	<b>17</b>

RESULT 3  
AAE26359  
ID AAE26359 standard; peptide; 17 AA

AA	13-DEC-2002 (first entry)
DT	
XX	
DE	Peptide related to myelin basic protein

KW Th2 immune response; myelin basic protein; MBP; vaccine; MS;  
KM multiple sclerosis; antisclerotic.

OS Unidentified.

PN US6379670-B1.  
YY

PD 30-APR-2002

PF 19-AUG-1999; 99US-00378244.  
VY

PR	18-NOV-1994;	94US-00342408.
PR	20-AUG-1998;	98US-00137759.

PA (NEUR-) NEUROCRINE BIOSCIENCE

XX

XX

XX  
E  
DE

PT administering the MHA  
PT Multiple sclerosis

XX Disclosure: Col 35-36: 49pp: English  
PS

CC The present invention

CC patient. The method involves administering a composition comprising the  
CC MBP peptide analogue CGP 77116 (NBI-57188). The method is useful for  
CC treating multiple sclerosis (MS). Sequences of the invention are also  
CC used as vaccines. The present sequence is a peptide related to human MBP

AA Sequence 17 AA:

Query Match	100.0%	Score 94	DB 5	Length 17
Best Local Similarity	100.0%	Pred. NC	6.1e-09	
Matches 17, Conservative	0	Mismatches	0	Indels 0
				Gaps 0

Qy	Qy
1	1
ENPVVHFFKNIIVTRPT	ENPVVHFFKNIIVTRPT
17	17
1	1
ENPVVHFFKNIIVTRPT	ENPVVHFFKNIIVTRPT
17	17

RESULT 4	
AAE23935	
ID	AAE23935 standard; peptide; 17 AA

AC AAE23935;  
XX

DT 10-SEP-2002 (first entry)  
XX Peptide analogue used in the invention.  
DE Autoimmune disease; multiple sclerosis; MS; Jbeta; Cbeta; Vbeta; Dbeta;  
XX immunosuppressive; T-cell receptor; therapy.  
KW Unidentified.  
XX WO200216434-A1.  
XX 28-FEB-2002.  
PD 22-AUG-2000; 2000WO-US022988.  
XX 22-AUG-2000; 2000WO-US022988.  
PR (BAYU ) BAYLOR COLLEGE MEDICINE.  
XX Zhang JZ;  
PI WPI; 2002-454317/48.  
DR A novel peptide used in the treatment of autoimmune disease e.g. multiple  
XX sclerosis.  
PT Example 2; Fig 2; 64pp; English.  
XX  
PS The invention relates to a peptide used in the treatment of autoimmune  
CC disease e.g. multiple sclerosis (MS). More particularly, it concerns a T-  
CC cell receptor sequence found in some MS patients and methods for its  
CC detection. T cell receptors comprise alpha and beta chains, with beta  
CC chains comprising the following regions from N-terminus to C-terminus:  
CC Vbeta-Jbeta-Cbeta. T cell receptors naturally vary in the Vbeta-  
CC Dbeta-Jbeta region. The peptides of the invention are used for treating  
CC autoimmune disease e.g multiple sclerosis. The present sequence is a  
CC peptide analogue used in the exemplification of the invention  
XX  
SQ Sequence 17 AA;  
Query Match 100.0%; Score 94; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVHFFKNIVTPRTP 17  
DB 1 ENPVHFFKNIVTPRTP 17  
RESULT 5  
ABP97941  
ID ABP97941 standard; peptide; 17 AA.  
XX  
AC ABP97941;  
XX  
DT 17-JUN-2003 (first entry)  
XX  
DE Amino acid sequence of a glycopeptide.  
XX  
KW Glycopeptide; serum; immunosorption column; antibody;  
XX multiple sclerosis.  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Modified-site 1 /note= "H attached"  
FT Modified-site 2 /note= "glycosylated residue"  
FT Modified-site 17 /note= "OH attached"  
XX  
PN WO2003009887-A2.

XX  
PD 06-FEB-2003.  
XX  
XX 25-JUL-2002; 2002WO-EP008274.  
PF 25-JUL-2001; 2001IT-FI000144.  
PR (UYFI-) UNIV FIRENZE.  
XX  
XX Pinto F, Papini AM, Chelli M, Rovero P, Lollì F;  
XX WPI; 2003-312632/30.  
DR  
XX  
XX Immunosorption column, useful for treating multiple sclerosis, contains  
PT glycopeptides able to react with disease-specific autoantibodies.  
XX  
PS Claim 4; Page 6; 13pp; English.  
XX  
XX ABP97937-44 represent glycopeptides of a formula given in the  
CC specification. The glycopeptides are used to produce columns of the  
CC invention. The specification describes immunosorption columns,  
CC containing conjugates comprising glycopeptides which are able to  
CC recognize antibodies implicated in multiple sclerosis. The column removes  
CC harmful antibodies selectively, leaving all other components of the serum  
CC unchanged. The column is used to treat multiple sclerosis  
XX  
SQ Sequence 17 AA;  
Query Match 100.0%; Score 94; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVHFFKNIVTPRTP 17  
DB 1 ENPVHFFKNIVTPRTP 17  
RESULT 6  
ABR56063  
ID ABR56063 standard; peptide; 17 AA.  
XX  
XX ABR56063;  
XX  
DT 06-AUG-2003 (first entry)  
XX  
DE Glycopeptide #5 for diagnosis and treatment of multiple sclerosis.  
XX  
KW Glycopeptide; neuroprotective; autoantibody; multiple sclerosis.  
XX  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Modified-site 2 /note= "Asn(Glc)"  
FT  
XX  
XX WO2003000733-A2.  
XX  
PD 03-JAN-2003.  
XX  
XX 19-JUN-2002; 2002WO-EP006767.  
PF 22-JUN-2001; 2001IT-FI000114.  
PR (UYFI-) UNIV FIRENZE.  
XX  
XX Papini AM, Chelli M, Rovero P, Lollì F;  
XX WPI; 2003-354383/33.  
DR  
XX  
XX Novel glycopeptides comprising a specific tetrapeptide, useful as  
PT diagnostic tools for identifying multiple sclerosis.  
XX  
XX Claim 7; Page 12; 14pp; English.  
PS

XX The present invention relates to glycopeptides (ABR56059-ABR56066). The  
CC glycopeptides have high specificity in recognizing autoantibodies  
CC involved in multiple sclerosis pathology, and thus are effectively used  
CC in diagnosis and treatment for multiple sclerosis  
XX  
SQ Sequence 17 AA:  
Query Match 100.0%; Score 94; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
1 ENPVVHFFKNIVTPRTP 17  
Db 1 ENPVVHFFKNIVTPRTP 17  
RESULT 7  
AA019672  
ID AA019672 standard; peptide; 17 AA.  
XX  
AC AA019672;  
XX  
DE 28-MAR-2003 (first entry)  
XX  
DE Human myelin basic protein MBP minimal epitope.  
XX  
XX Human; Ig; immunoglobulin; immunotherapy; immune disease; MBP;  
XX Fc epsilon receptor; autoimmune disease; constant region; heavy chain;  
XX antihistaminic; antiallergic; antiinflammatory; dermatological; G2;  
XX antitachycardic; antineuritic; antidiabetic; neuroprotective;  
XX myelin basic protein; minimal epitope.  
XX  
XX Homo sapiens.  
XX  
XX WO20028317-A2.  
XX  
XX 07-NOV-2002.  
XX  
XX 01-MAY-2002; 2002WO-US013527.  
XX  
XX 01-MAY-2001; 2001US-00847208.  
XX  
XX 24-OCT-2001; 2001US-00000439.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Saxon A, Zhang K, Zhu D;  
XX  
XX MPI; 2003-103456/09.  
XX  
XX New fusion molecules comprising polypeptide sequences that bind to IgG  
XX inhibitory receptor and native IgG receptor, useful for treating IgG-  
XX mediated hypersensitivity reactions, e.g. asthma or allergies, or  
XX autoimmune diseases.  
XX  
XX Claim 23; Page 116; 116pp; English.  
XX  
XX The present invention relates to a fusion molecule comprising a first  
XX polypeptide sequence capable of specific binding to a native IgG  
XX inhibitory receptor consisting of an immune receptor tyrosine-based  
XX inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,  
XX functionally connected to a second polypeptide sequence capable of  
XX (Fc epsilon) binding directly or indirectly to a native IgG receptor  
XX (Fc epsilon). Also provided are nucleotide sequences encoding such a  
XX fusion protein. The fusion molecules and compositions are useful for  
XX treating an IGE-mediated biological response, preferably an IGE-mediated  
XX hypersensitivity reaction, such as asthma, allergic rhinitis, atopic  
XX dermatitis, severe food allergies, chronic urticaria, angioedema or  
XX anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,  
XX type-I diabetes mellitus, or multiple sclerosis, and for preventing of,  
XX or symptoms resulting from, a type I hypersensitivity reaction in a  
XX subject receiving immunotherapy. The present sequence is the human myelin  
XX basic protein minimal epitope which can be used in a fusion protein of

CC the invention  
XX  
SQ Sequence 17 AA:  
Query Match 100.0%; Score 94; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
1 ENPVVHFFKNIVTPRTP 17  
Db 1 ENPVVHFFKNIVTPRTP 17  
RESULT 8  
ADE50773  
ID ADE50773 standard; peptide; 17 AA.  
XX  
AC ADE50773;  
XX  
DE 29-JAN-2004 (first entry)  
XX  
DE Wild-type human myelin basic protein peptide analog.  
XX  
XX Human; Th2; immune response; myelin basic protein; peptide analog;  
XX proteolysis; multiple sclerosis; neuroprotective; gene therapy.  
XX  
XX Homo sapiens.  
XX  
XX US2002176866-A1.  
XX  
XX 28-NOV-2002.  
XX  
XX 20-MAR-2002; 2002US-00104973.  
XX  
XX 18-NOV-1994; 94US-00342408.  
XX  
XX 20-AUG-1998; 98US-00137759.  
XX  
XX 19-AUG-1999; 99US-00378244.  
XX  
XX (NEUR-) NEUROCRINE BIOSCIENCES INC.  
XX  
XX Gaur A, Conlon P, Ling NC, Staehelin T, Crowe PD;  
XX  
XX MPI; 2003-615722/58.  
XX  
XX Inducing a Th2 immune response to myelin basic protein or its peptide  
XX analog in a patient, useful for treating multiple sclerosis, comprises  
XX administering an amount of a pharmaceutical composition comprising a  
XX peptide analog.  
XX  
XX Disclosure, SEQ ID NO 3; 52pp; English.  
XX  
XX The invention discloses a method for inducing a Th2 immune response to  
XX myelin basic protein or its peptide analog in a patient, comprising  
XX administering a composition comprising a peptide analog in combination  
XX with a carrier/adjuvant or diluent. The peptide analog comprises at least  
XX 7 amino acids selected from residues 83 to 99 of human myelin basic  
XX protein, where: the L-lysine at position 91, L-arginine at position 97 or  
XX L-threonine at position 95, is altered to another amino acid, and one to  
XX three L-amino acids selected from valine at position 86 or 87, histidine  
XX at position 88, threonine at position 95 or 98, and proline at position  
XX 99 are altered to an amino acid other than the amino acid present in the  
XX native protein at that position or the L-lysine at position 91 is altered  
XX to another amino acid and the N- and/or C-terminal amino acid are altered  
XX to another amino acid, such that upon administration of the peptide  
XX analog in vivo proteolysis is reduced. The peptide analog comprises 7-17  
XX amino acids and one to four additional altered residues. The N-terminal  
XX amino acid is residue 83 of human myelin basic protein. At least one of  
XX the additional L-amino acids selected from residues 83 to 90 and 92 to 99  
XX is substituted with a charged amino acid. The method is useful for  
XX treating multiple sclerosis using peptide analogs of human myelin basic  
XX protein. The sequence presented is the wild-type human myelin basic  
XX protein peptide analog.



SO Sequence 17 AA;  
Query Match 100.0%; Score 94; DB 7; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
1 ENPVVHFFKNIVTPRTP 17  
DB 1 ENPVVHFFKNIVTPRTP 17  
RESULT 9  
ADK67704  
ADK67704 standard; peptide; 17 AA.  
AC ADK67704;  
XX  
XX  
XX 06-MAY-2004 (first entry)  
DT  
DE Human myelin basic protein peptide fragment MBP-1 (aa110-126).  
XX  
XX Human; myelin basic protein; vaccine; multiple sclerosis; T cell.  
XX Homo sapiens.  
XX WO2004015070-A2.  
XX 19-FEB-2004.  
PD 06-AUG-2003; 2003WO-US024548.  
XX 08-AUG-2002; 2002US-0402521P.  
PR (BAYU) BAYLOR COLLEGE MEDICINE.  
PA (OPEX-) OPEXA PHARM INC.  
XX Zhang JZ;  
PI  
XX WPI; 2004-180654/17.  
DR  
XX Isolating one or more T cells specific for an antigen of interest  
PT comprises incubating a T cell sample with an antigen, useful for  
PT diagnosing or treating multiple sclerosis, psoriasis, thyroiditis,  
PT diabetes and rheumatoid arthritis.  
XX  
XX Example 1; SEQ ID NO 1; 38pp; English.  
PS  
XX The present invention is direct to methods of isolating antigen specific  
CC T cells, especially T cells specific for self or autoantigens. This  
CC comprises incubating a sample of T cells obtained from a patient with the  
CC antigen and selecting T cells that express one or more of first markers  
CC selected from CD63, CD4, CD25, CD36 and HLA-DR, and one or more second  
CC markers selected from interleukin-2, interferon-gamma, tumour necrosis  
CC factor alpha, interleukin-5, interleukin-10 and interleukin-12. The  
CC methods are useful for isolating autoreactive T cells which play a role  
CC in the pathogenesis of autoimmune diseases. The methods also permit the  
CC diagnosis of autoimmune disease as well as monitoring the progression of  
CC the disease and for monitoring the efficacy of treatment. The methods  
CC allow the preparation of autologous T cell vaccines for the treatment of  
CC T cell related autoimmune diseases. Vaccine preparation involves the  
CC isolation of antigen-specific T cells optionally followed by culturing  
CC steps which allow the expansion of the population of isolated antigen-  
CC specific T cells. An example from the invention describes the isolation  
CC of myelin-reactive T cells for T cell vaccination. Peripheral blood  
CC mononuclear cells were isolated from the blood of multiple sclerosis  
CC patients and incubated with peptides comprising known immunodominant  
CC regions of 3 myelin proteins. These included the present peptide, which  
CC comprises amino acids 110-126 of human myelin basic protein. Cells were  
CC then selected for the expression of gene products indicative of activated  
CC T cells, and myelin-reactive T cells were propagated in culture. The  
CC methods and compositions of the invention are useful for the diagnosis  
CC and/or treatment of autoimmune diseases or T cell associated conditions  
CC such as multiple sclerosis, myasthenia gravis, psoriasis, systemic lupus

CC erythematous, autoimmune thyroiditis, Grave's disease, inflammatory  
CC bowel disease, diabetes and rheumatoid arthritis.  
XX  
XX  
SO Sequence 17 AA;  
Query Match 100.0%; Score 94; DB 8; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ENPVVHFFKNIVTPRTP 17  
1 ENPVVHFFKNIVTPRTP 17  
DB 1 ENPVVHFFKNIVTPRTP 17  
RESULT 10  
ADL18291  
ADL18291 standard; peptide; 17 AA.  
AC ADL18291;  
XX  
XX 20-MAY-2004 (first entry)  
DT  
DE Human myelin basic protein (MBP), peptide #2.  
XX  
XX Demyelinating disease; neuron-specific antigen; human;  
XX myelin basic protein; MBP; myelin oligodendrocyte glycoprotein;  
XX myelin associated glycoprotein; MAG; proteolipid protein; PLP;  
XX small heat shock protein; transthyretin; glial fibrillary protein;  
XX S-100 protein; cross-reactive peptide; glutamate receptor;  
XX phosphodiesterase; multiple sclerosis.  
XX  
XX Homo sapiens.  
OS  
XX  
XX US2004043431-A1.  
XX 04-MAR-2004.  
PD 29-AUG-2002; 2002US-00233892.  
XX 29-AUG-2002; 2002US-00233892.  
PR (VOUD/) VOUDANI A.  
XX  
XX Vojdani A;  
PI  
XX WPI; 2004-313756/29.  
DR  
XX Diagnosing likelihood and severity of demyelinating disease, by  
PT determining antibodies against neuron-specific antigen, comparing level  
PT of detected antibodies with normal level for detecting absence/likelihood  
PT of demyelinating disease.  
XX  
XX Claim 6; SEQ ID NO 2; 27pp; English.  
PS  
XX The present invention relates to a method of diagnosing the likelihood  
CC and severity of demyelinating diseases. The method involves determining  
CC antibodies against neuron-specific antigen in sample, comparing the level  
CC of antibodies with the normal level of antibodies, where normal level of  
CC antibodies for neuron-specific antigen indicate optimal conditions, lower  
CC than or higher than normal level of antibodies for the antigen indicate  
CC an absence of or a likelihood of demyelinating diseases, respectively.  
CC The neuron-specific antigen is chosen from myelin basic protein (MBP),  
CC myelin oligodendrocyte glycoprotein, myelin associated glycoprotein  
CC (MAG), proteolipid protein (PLP), small heat shock protein,  
CC transthyretin, glial fibrillary protein, S-100 protein, cross-reactive  
CC peptide from dietary protein, cross-reactive peptide from infectious  
CC agent, glutamate receptor, and phosphodiesterase. The immunoassay is an  
CC enzyme linked immunosorbent assay (ELISA) test. The method is useful for  
CC diagnosing the likelihood and severity of demyelinating diseases such as  
CC multiple sclerosis in a patient. The present sequence represents a  
CC peptide from human MBP.  
XX  
XX Sequence 17 AA;

Query Match 100.0%; Score 94; DB 8; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
 |||||  
 DB 1 ENPVVHFFKNIVTPRTP 17

## RESULT 11

AA44116  
 ID AAR44116 standard; peptide; 17 AA.  
 XX  
 AC AAR44116;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 09-MAY-1994 (first entry)  
 XX  
 DE Human myelin basic protein residues 86-102.  
 XX  
 KW hMBP; suppression; auto immune response; multiple sclerosis;  
 KW immunodominant epitope; T-cell proliferation; CD4; T-cells.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9321222-A1.  
 XX  
 PD 28-OCT-1993.  
 XX  
 PF 09-APR-1993; 93WO-US003369.  
 XX  
 PR 09-APR-1992; 92US-00865318.  
 XX  
 XX

## (AUTO-) AUTOIMMUNE INC.

Weiner HL, Haefler DA, Miller A, Al-Sabbagh A;

WPI; 1993-351657/44.

PT New peptide(s) derived from human myelin basic protein - used for  
 PT suppressing auto-immune response, partic. in treating multiple sclerosis.

PS Claim 1; Page 29; 118pp; English.

XX The peptide represents residues 86-102 of human myelin basic protein  
 CC (hMBP). The fragment comprises an immunodominant epitope of hMBP which  
 CC was identified by overlapping 20-mer oligopeptide sequence analysis using  
 CC T-cell line assays. The peptide can be used to stop proliferation of  
 CC human T-cells specific for MBP or to elicit active suppression of such T-  
 CC cells. They are also used partic. for the treatment of multiple  
 CC sclerosis. The peptide is also useful for identifying CD4+ T-cells  
 CC reactive with MBP. See also AAR44114-25. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX

## SQ Sequence 17 AA.

Query Match 94.7%; Score 89; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NPVVFHFFKNIVTPRTP 17  
 |||||  
 DB 1 NPVVFHFFKNIVTPRTP 16

## RESULT 12

AA95360  
 ID AAR95360 standard; peptide; 17 AA.  
 XX  
 AC AAR95360;  
 XX  
 DT 16-DEC-1996 (first entry)  
 XX

XX Residues 84-100 of myelin basic protein.  
 XX

XX Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE;  
 KW CD4+; T-cell; autoimmune disease; demyelination; central nervous system;  
 KW CNS; animal model; human; multiple sclerosis; MS; mammal; benign MS; MOG;  
 KW relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP;  
 KW diabetes; Graves disease; myasthenia gravis; Good Pasture's syndrome;  
 KW psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG;  
 KW myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.  
 XX

## Synthetic.

OS  
 XX  
 PN WO9612737-A2.  
 XX  
 PD 02-MAY-1996.  
 XX  
 PF 25-OCT-1995; 95WO-US013682.  
 XX  
 PR 25-OCT-1994; 94US-00328224.  
 PR 15-MAR-1995; 95US-00404228.  
 XX  
 PA (IMMU-) IMMUNOLOGIC PHARM CORP.

PI Smilek D, Samson M, Gelfer M, Hsu D, Shi J, Paliard X, Devaux B;  
 PI Rothbard J, Franzen H;  
 XX  
 DR WPI; 1996-230552/23.

PT Myelin basic derived peptide(s) and analogs - used in the treatment of  
 PT Multiple Sclerosis, psoriasis, Graves Disease, etc.  
 XX

PS Claim 8; Fig 14; 91pp; English.

XX AAR95334-R95374 represent peptides derived from myelin basic protein  
 CC (MBP). Immunisation with MBP can be used to induce experimental allergic  
 CC encephalomyelitis (EAE) in susceptible strains of mice. EAE is a CD4+ T-  
 CC cell mediated autoimmune disease which results in demyelination of the  
 CC central nervous system, resulting in paralysis and other neurological  
 CC abnormalities. EAE is a commonly used animal model for human multiple  
 CC sclerosis (MS). These sequences can be used in compositions for treating  
 CC MS in a mammal. The composition acts to down regulate the autoimmune  
 CC response, and may be administered in an amount sufficient to prevent the  
 CC onset of symptoms of MS. The compositions may also be used to treat  
 CC advanced stage MS, especially relapsing-remitting MS, chronic progressive  
 CC MS or benign MS. These peptides may also be used in the treatment of  
 CC other diseases involving myelin autoantigens, including diabetes, Graves  
 CC disease, myasthenia gravis, Good Pasture's syndrome, psoriasis,  
 CC thyroiditis, and rheumatoid arthritis. Peptides derived from other myelin  
 CC autoantigens, such as myelin oligodendrocyte protein (MOG), proteolipid  
 CC protein (PLP), and myelin associated glycoprotein (MAG) can be used as  
 CC alternatives to these MBP peptides in these compositions  
 XX

## SQ Sequence 17 AA.

Query Match 94.7%; Score 89; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NPVVFHFFKNIVTPRTP 17  
 |||||  
 DB 1 NPVVFHFFKNIVTPRTP 16

## RESULT 13

AAW73601  
 ID AAW73601 standard; peptide; 17 AA.  
 XX  
 AC AAW73601;  
 XX  
 DT 18-MAR-1999 (first entry)  
 XX  
 DE Human myelin basic protein fragment.

encephalogenic proteins and peptides.";

Science 179:478-480(1973).

-1- FUNCTION: Is, with PIP, the most abundant protein component of the myelin membrane in the CNS. Has a role in both the formation and stabilization of this compact multilayer arrangement of bilayers.

Each splice variant and charge isomer may have a specialized function in the assembly of an optimized, biochemically functional myelin membrane (By similarity).

-1- SUBUNIT: Homodimer (By similarity).

-1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.

-1- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=4;

Comment=Additional isoforms seem to exist;

Name=1; Synonyms=21.5 kDa;

IsoId=P02688-1; Sequence=Displayed;

Name=2; Synonyms=18.5 kDa;

IsoId=P02688-2; Sequence=VSP\_003321;

Name=3; Synonyms=17 kDa;

IsoId=P02688-3; Sequence=VSP\_003322;

Name=4; Synonyms=14 kDa;

IsoId=P02688-4; Sequence=VSP\_003321; VSP\_003322;

-1- TISSUE SPECIFICITY: Found in both the central and the peripheral nervous system.

-1- PTM: As in other animals, several charge isomers may be produced as a result of optional posttranslational modifications, such as phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.

-1- PTM: Arg-130 was found to be 44% monomethylated and 11% symmetrically dimethylated.

-1- SIMILARITY: Belongs to the myelin basic protein family.

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EMBL; AJ132895; CA10804.1; -;

EMBL; AJ132896; CA10805.1; -;

EMBL; AJ132897; CA10806.1; -;

EMBL; AJ132898; CA10807.1; -;

EMBL; M25889; AAA1575.1; -;

EMBL; K00512; -; NOT\_ANNOTATED\_CDS.

EMBL; X72392; -; NOT\_ANNOTATED\_CDS.

PIR; B24351; MBRTS.

HSSP; P02686; IQCL.

DR RGD; 3054; MBP.

InterPro: IPR000548; Myelin BP.

DR Pfam; PF01669; Myelin\_MBP; I.

DR PRINTS; PR00212; MYELINBP.

DR ProDom; PD004542; Myelin\_BP; 1.

DR PROSITE; PS00569; MYELIN\_MBP; 1.

Acetylation; Alternative splicing; Autoimmune encephalomyelitis; Citrullination; Direct protein sequencing; Methylation; Myelin; Phosphorylation; Structural protein.

KM Phosphorylation; Structural protein.

INIT\_MET 0 0

FT MOD\_RES 1 1 N-acetylalanine.

FT MOD\_RES 7 7 Phosphoserine (By similarity).

FT MOD\_RES 25 25 Citrulline (By similarity).

FT MOD\_RES 31 31 Citrulline (By similarity).

FT MOD\_RES 56 56 Phosphoserine (By similarity).

FT MOD\_RES 121 121 Phosphothreonine (By similarity).

FT MOD\_RES 126 126 Deamidated glutamine (partial) (By similarity).

FT MOD\_RES 130 130 Omega-N-methylarginine (partial).

FT MOD\_RES 130 130 Symmetric dimethylarginine (partial).

FT MOD\_RES 138 138 Phosphoserine (By similarity).

FT MOD\_RES 153 153 Citrulline (By similarity).

FT MOD\_RES 171 171 Deamidated glutamine (partial) (By similarity).

FT MOD\_RES 183 183 Citrulline (By similarity).

FT MOD\_RES 185 185 Phosphoserine (By similarity).

FT MOD\_RES 189 189 Phosphoserine (By similarity).

FT MOD\_RES 194 194 Citrulline (By similarity).

FT VARSPPLIC 59 84 Missing (in isoform 2 and isoform 4).

FT VARSPPLIC 140 180 /FTId=VSP\_003322.

FT VARSPPLIC 140 180 Missing (in isoform 3 and isoform 4).

FT CONFLICT 46 47 /FTId=VSP\_003322.

FT CONFLICT 191 191 SC -> GS (in Ref. 6).

FT CONFLICT 191 191 M -> I (in Ref. 1 and 3).

SEQ SEQUENCE 194 AA; 21371 MW; 68FB399C250B4C50 CRC64;

Query Match 100.0%; Score 94; DB 1; Length 194;

Best Local Similarity 100.0%; Pred. No. 1.6e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17

DB 106 ENPVVHFFKNIVTPRTP 122

RESULT 12

Q65ZS4 PRELIMINARY; PRT; 203 AA.

ID Q65ZS4

AC Q65ZS4;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Myelin basic protein.

DE Name=MBP;

GN Homo sapiens (Human).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=86259714; PubMed=2425357;

RA Kamholz J., de Ferreira F., Puckett C., Lazzarini R.;

RT Identification of three forms of human myelin basic protein by cDNA cloning";

RL Proc. Natl. Acad. Sci. U.S.A. 83:4962-4966(1986).

RL [2]

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=96128281; PubMed=8544862; DOI=10.1016/0161-5890(95)00066-6;

RA Nye S.H., Pelfrey C.M., Burkitt J.J., Voskuhl R.R., Lenardo M.J., Mueller J.P.;

RT "Purification of immunologically active recombinant 21.5 kDa isoform of human myelin basic protein.";

RT Mol. Immunol. 32:1131-1141(1995).

DR EMBL; LA1657; AAC1944.1; -;

DR EMBL; LA1657; AAC1944.1; -;

DR InterPro: IPR000548; Myelin BP.

DR Pfam; PF01669; Myelin\_MBP; I.

DR PRINTS; PR00212; MYELINBP.

DR ProDom; PD004542; Myelin\_BP; 1.

DR PROSITE; PS00569; MYELIN\_MBP; 1.

DR SEQUENCE 203 AA; 22316 MW; C21A7D718FC2D30F CRC64;

Query Match 100.0%; Score 94; DB 2; Length 203;

Best Local Similarity 100.0%; Pred. No. 1.6e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17

DB 110 ENPVVHFFKNIVTPRTP 126

RESULT 13

MBP\_MOUSE

ID MBP\_MOUSE STANDARD; PRT; 250 AA.

AC P04370; Q01585; Q03139; Q61835; Q61837; Q99KE4; Q9QWP1;

DT 20-MAR-1987 (Rel. 04, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)

- DE Myelin basic protein (MBP) (Myelin A1 protein).
- GN Name=Mbp, Synonyms=Shi;
- OS Mus musculus (Mouse).
- OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
- OX NCBI\_TaxId=10090;
- RA Amur-Umarje S., Landry C.F., Handley V.W., Newman S., Garbay B., Kikamura K.;
- RA "Structure and developmental regulation of Ggll1-amp, a 105-kilobase gene that encompasses the myelin basic protein gene and is expressed in cells in the oligodendrocyte lineage in the brain.";
- RL J. Biol. Chem. 268:4930-4938(1993).
- RC STRAIN=C57BL/6; TISSUE=Bone marrow;
- RC MEDLINE=93057537; PubMed=1279125;
- RA Grima B., Zelenik D., Pessac B.;
- RA "A novel transcript overlapping the myelin basic protein gene.";
- RT J. Neurochem. 59:2318-2323(1992).
- RA "Alternative splicing accounts for the four forms of myelin basic protein.";
- RL Cell 43:721-727(1985).
- RA "SEQUENCE FROM N.A. (ISOFORM 5)."
- RA MEDLINE=85254913; PubMed=2410136;
- RA Takahashi N., Roach A., Teglow D.B., Prusiner S.B., Hood L.E.;
- RT "Cloning and characterization of the myelin basic protein gene from mouse: one gene can encode both 14 kd and 18.5 kd MBPs by alternate use of exons.";
- RL Cell 42:139-148(1985).
- RA "SEQUENCE FROM N.A. (ISOFORMS 6 AND 7), AND SEQUENCE OF 9-194 FROM N.A."
- RC STRAIN=C57BL/6J; TISSUE=Brain;
- RC MEDLINE=87118269; PubMed=2433693;
- RA Newman S., Kikamura K., Campagnoni A.T.;
- RT "Identification of a cDNA coding for a fifth form of myelin basic protein in mouse.";
- RL Proc. Natl. Acad. Sci. U.S.A. 84:886-890(1987).
- RA "SEQUENCE FROM N.A. (ISOFORM 8)."
- RA PubMed=1692584;
- RA Kikamura K., Newman S.L., Campagnoni C.W., Verdi J.M., Mohandas T., Handley V.W., Campagnoni A.T.;
- RT "Expression of a novel transcript of the myelin basic protein gene.";
- RL J. Neurochem. 54:2032-2041(1990).
- RA "SEQUENCE FROM N.A. (ISOFORM 8)."
- RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
- RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
- RA Okazaki Y., Furuno M., Kasukawa T., Adachi U., Bono H., Kondo S., Nakido I., Oato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gyojibori T., Balarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schimi L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Fraser K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Guettnich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konegaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Malais K., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pereira G., Pesole G., Petrovsky N., Pillai R., Pontius U.U., Qi D., Ramchandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandel A., Schneider C., Sempie C.A., Setou M., Shinada K., Sultana K., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wegner T., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wyszynski B., Yanagisawa M., Yano I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai U., Aizawa K., Arikawa T., Fukuda S., Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A., Yasuniishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney B., Hayashizaki Y.;
- RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
- RL Nature 420:563-573(2002).
- RA "SEQUENCE FROM N.A. (ISOFORM 9)."
- RC TISSUE=Breast tumor;
- RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
- RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen S.J., Bosak S.A., McEwan P.J., McKernan K.D., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
- RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
- RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
- RA "SEQUENCE OF 135-157 FROM N.A."
- RC MEDLINE=89252919; PubMed=2470651; DOI=10.1016/0378-1119(89)90380-6;
- RA Miura M., Tamura T.A., Aoyama A., Mikoshiba K.;
- RT "The promoter elements of the mouse myelin basic protein gene function efficiently in NG108-15 neuronal/911a1 cells.";
- RL Gene 75:31-38(1989).
- RA "PARTIAL SEQUENCE FROM N.A. (ISOFORMS 4; 6 AND 9)."
- RC MEDLINE=86259714; PubMed=2425357;
- RA Kamholz J., de Ferreira F., Puckett C., Lazzerini R.A.;
- RT "Identification of three forms of human myelin basic protein by cDNA cloning.";
- RL Proc. Natl. Acad. Sci. U.S.A. 83:4962-4966(1986).
- RA "SEQUENCE OF 193-222 FROM N.A."
- RC MEDLINE=84119431; PubMed=6198644;
- RA Zeller N.K., Hunkeler M.J., Campagnoni A.T., Sprague J., Lazzerini R.A.;
- RT "Characterization of mouse myelin basic protein messenger RNAs with a myelin basic protein cDNA clone.";
- RL Proc. Natl. Acad. Sci. U.S.A. 81:18-22(1984).
- RA "PARTIAL SEQUENCE FROM N.A. (ISOFORMS 10 AND 11)."
- RC TISSUE=Spinal cord;
- RC MEDLINE=91162193; PubMed=1705957;
- RA Aruga J., Okano H., Mikoshiba K.;
- RT "Identification of the new isoforms of mouse myelin basic protein: the existence of exon 5a.";
- RL J. Neurochem. 56:1222-1226(1991).
- RA "PARTIAL SEQUENCE FROM N.A. (ISOFORMS 12 AND 13)."
- RC TISSUE=Embryonic brain;
- RC MEDLINE=93203893; PubMed=7681106;





Search completed: June 7, 2005, 09:01:30  
Job time : 10.3679 secs

```
RL G1a 2:241-249(1989).
CC -1- FUNCTION: Is, with PLP, the most abundant protein component of the
CC myelin membrane in the CNS. Has a role in both the formation and
CC stabilization of this compact multilayer arrangement of bilayers.
CC Each splice variant and charge isomer may have a specialized
CC function in the assembly of an optimized, biochemically functional
CC myelin membrane (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=PI5720-1; Sequence=Displayed;
CC Note=Major isoform;
CC Name=2;
CC IsoId=PI5720-2; Sequence=VSP_003323;
CC -1- DEVELOPMENTAL STAGE: In the optic lobe, first detected at
CC embryonic day 14. Expression strongly increases between embryonic
CC days 16 and 18, reaches a maximum at postnatal day 1, and then
CC declines again to the adult level.
CC -1- PTM: As in other animals, several charge isomers may be produced
CC as a result of optional posttranslational modifications, such as
CC phosphorylation of serine or threonine residues, deamidation of
CC glutamine or asparagine residues, citrullination and methylation
CC of arginine residues.
CC -1- SIMILARITY: Belongs to the myelin basic protein family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X17103; CAA34959.1; -.
CC DR PIR: S08535; S08535.
CC DR HSSP: P02686; 1QCL.
CC DR InterPro: IPR000548; Myelin_BP.
CC DR Pfam: PF01669; Myelin_MBP; 1.
CC DR ProDom: PD004542; Myelin_BP; 1.
CC DR PRINTS: PR00212; MYELINMBP.
CC DR PROSITE: PS00569; MYELIN_MBP; 1.
CC KW Acetylation; Alternative splicing; Citrullination; Methylation;
CC Myelin; Phosphorylation; Structural protein.
CC FT INIT MET 0 0
CC FT MOD_RES 1 1 N-acetylalanine (By similarity).
CC FT MOD_RES 7 7 Phosphoserine (By similarity).
CC FT MOD_RES 24 24 Citrulline (By similarity).
CC FT MOD_RES 29 29 Citrulline (By similarity).
CC FT MOD_RES 96 96 Phosphothreonine (By similarity).
CC FT MOD_RES 101 101 Deamidated glutamine (partial) (By
CC similarity).
CC FT MOD_RES 105 105 Deamidated glutamine (partial) (By
CC similarity).
CC FT MOD_RES 113 113 Symmetric dimethylarginine (By
CC similarity).
CC FT MOD_RES 146 146 Phosphoserine (By similarity).
CC FT MOD_RES 164 164 Deamidated glutamine (partial) (By
CC similarity).
CC FT MOD_RES 168 168 Phosphoserine (By similarity).
CC FT MOD_RES 173 173 Phosphoserine (By similarity).
CC FT MOD_RES 173 173 Citrulline (By similarity).
CC FT MOD_RES 173 173 Citrulline (in isoform 2).
CC FT VARSPLC 104 114 Missing (in isoform 2).
CC FT VARSPLC 104 114 /FTId=VSP_003323.
CC SQ SEQUENCE 173 AA; 18677 MW; ABFE70D4C9CF019D CRC64;
CC
CC Query Match 92.6%; Score 87; DB 1; Length 173;
CC Best Local Similarity 88.2%; Pred. No. 2.1e-06;
CC Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 EMPVVFHFKNIIVTPRTP 17
CC DB 81 DNPVVFHFKNIIVSPRTP 97
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OM protein - protein search, using sw model

Run on: June 7, 2005, 09:37:21 ; Search time 143 Seconds  
(without alignments)  
42.821 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94

Sequence: 1 ENPVVHFFKNIVTPRTP 17

Scoring table: BLOSUM62

Searched: 1599520 seqs, 360203123 residues

Total number of hits satisfying chosen parameters: 263935

Minimum DB seq length: 0

Maximum DB seq length: 17

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
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- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	100.0	17	US-10-104-973-3	Sequence 3, Appl1
2	94	100.0	17	US-10-000-439-13	Sequence 13, Appl1
3	94	100.0	17	US-10-362-264-1	Sequence 1, Appl1
4	94	100.0	17	US-10-233-892A-2	Sequence 2, Appl1
5	94	100.0	17	US-10-482-044-5	Sequence 5, Appl1
6	87	92.6	17	US-09-813-463A-13	Sequence 13, Appl1
7	87	92.6	17	US-09-813-463A-13	Sequence 13, Appl1
8	82	87.2	15	US-09-909-460-37	Sequence 37, Appl1
9	82	87.2	15	US-09-847-172-41	Sequence 41, Appl1
10	82	87.2	15	US-09-872-836-37	Sequence 37, Appl1
11	82	87.2	15	US-09-739-466C-5	Sequence 5, Appl1
12	82	87.2	15	US-10-152-654-11	Sequence 11, Appl1

13	82	87.2	15	14	US-10-056-583-1	Sequence 1, Appl1
14	82	87.2	15	14	US-10-239-313A-142	Sequence 142, App
15	82	87.2	15	14	US-10-362-264-5	Sequence 5, Appl1
16	82	87.2	15	15	US-10-404-679-11	Sequence 11, Appl1
17	82	87.2	15	15	US-10-406-783-1	Sequence 1, Appl1
18	82	87.2	15	15	US-10-406-783-2	Sequence 2, Appl1
19	82	87.2	15	16	US-10-617-568-26	Sequence 26, Appl1
20	79	84.0	15	14	US-10-056-583-69	Sequence 69, Appl1
21	79	84.0	15	14	US-10-239-313A-144	Sequence 144, App
22	79	84.0	15	14	US-10-239-313A-145	Sequence 145, App
23	78	83.0	15	14	US-10-239-313A-125	Sequence 125, App
24	78	83.0	15	14	US-10-239-313A-126	Sequence 126, App
25	78	83.0	15	14	US-10-239-313A-136	Sequence 136, App
26	78	83.0	15	14	US-10-239-313A-137	Sequence 137, App
27	77	81.9	15	14	US-10-239-313A-134	Sequence 134, App
28	77	81.9	15	14	US-10-239-313A-138	Sequence 138, App
29	77	81.9	15	14	US-10-239-313A-141	Sequence 141, App
30	77	81.9	15	14	US-10-362-264-4	Sequence 4, Appl1
31	76	80.9	14	13	US-10-015-540-3	Sequence 3, Appl1
32	76	80.9	15	14	US-10-239-313A-127	Sequence 127, App
33	76	80.9	15	14	US-10-239-313A-132	Sequence 6, Appl1
34	76	80.9	15	14	US-10-362-264-6	Sequence 6, Appl1
35	76	80.9	15	16	US-10-617-568-27	Sequence 27, Appl1
36	76	80.9	15	16	US-10-103-395-3	Sequence 3, Appl1
37	76	80.9	16	13	US-10-149-138-4381	Sequence 4381, Ap
38	76	80.9	16	15	US-10-149-135-2321	Sequence 2321, Ap
39	76	80.9	16	16	US-10-149-138-4381	Sequence 4381, Ap
40	76	80.9	16	16	US-10-149-138-4381	Sequence 4381, Ap
41	76	80.9	17	16	US-10-475-706-4	Sequence 4, Appl1
42	75	79.8	17	13	US-10-104-973-6	Sequence 6, Appl1
43	74	78.7	15	14	US-10-239-313A-118	Sequence 118, App
44	74	78.7	15	14	US-10-239-313A-130	Sequence 130, App
45	74	78.7	15	14	US-10-239-313A-131	Sequence 131, App

#### ALIGNMENTS

RESULT 1  
US-10-104-973-3  
Sequence 3, Application US/10104973  
Publication No. US20020176866A1  
GENERAL INFORMATION:  
APPLICANT: Gaur, Amitabh  
APPLICANT: Conlon, Paul J.  
APPLICANT: Ling, Nicholas C.  
APPLICANT: Staehlin, Theophil  
TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING  
TITLE OF INVENTION: PEPTIDE ANALOGS OF HUMAN MYELIN BASIC PROTEIN  
FILE REFERENCE: 690068.405C4  
CURRENT APPLICATION NUMBER: US/10104,973  
CURRENT FILING DATE: 2002-03-20  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Solid Phase  
US-10-104-973-3

Query Match 100.0%; Score 94; DB 13; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.6e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17  
DB 1 ENPVVHFFKNIVTPRTP 17

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RESULT 2
US-10-000-439-13
; Sequence 13, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; FILE REFERENCE: UC067.004A
; CURRENT APPLICATION NUMBER: US/10/000,439
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/847,208
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-439-13

Query Match          100.0%; Score 94; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 4,6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ENPVVHFFKNIVTPRTP 17
DB      1 ENPVVHFFKNIVTPRTP 17

RESULT 3
US-10-362-264-1
; Sequence 1, Application US/10362264
; Publication No. US20030191063A1
; GENERAL INFORMATION:
; APPLICANT: Wraith, David
; APPLICANT: Anderson, Stephen
; APPLICANT: Mazza, Graziella
; APPLICANT: Ponsford, Mary
; APPLICANT: Streeter, Heather
; APPLICANT: The University of Bristol
; TITLE OF INVENTION: PEPTIDE SELECTION METHOD
; FILE REFERENCE: 1433 004US1
; CURRENT APPLICATION NUMBER: US/10/362,264
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/GB01/03702
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 0020618.5
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 0114547.3
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-362-264-1

Query Match          100.0%; Score 94; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 4,6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ENPVVHFFKNIVTPRTP 17
DB      1 ENPVVHFFKNIVTPRTP 17

RESULT 4
US-10-233-892A-2
; Sequence 2, Application US/10233892A
; Publication No. US20040043431A1
; GENERAL INFORMATION:
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; APPLICANT: Vojdani, Aristo
; TITLE OF INVENTION: DIAGNOSIS OF MULTIPLE SCLEROSIS AND
; FILE REFERENCE: IMSMS.001A
; CURRENT APPLICATION NUMBER: US/10/233,892A
; CURRENT FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Myelin Binding Protein Sequence 83-89
US-10-233-892A-2

Query Match          100.0%; Score 94; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 4,6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ENPVVHFFKNIVTPRTP 17
DB      1 ENPVVHFFKNIVTPRTP 17

RESULT 5
US-10-482-044-5
; Sequence 5, Application US/10482044
; Publication No. US20040235713A1
; GENERAL INFORMATION:
; APPLICANT: Anna Maria PAPINI et al
; TITLE OF INVENTION: Glycopeptides, their preparation and use in the diagnosis or
; FILE REFERENCE: 2784 PTWO
; CURRENT APPLICATION NUMBER: US/10/482,044
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: PCT/EP 02/06767
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: FI2001A000114
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: glycopeptide
; NAME/KEY: CARBOHYD
; LOCATION: (2)..(2)
; OTHER INFORMATION: the carbohydrate is beta-D-glucopyranosyl
US-10-482-044-5

Query Match          100.0%; Score 94; DB 16; Length 17;
Best Local Similarity 100.0%; Pred. No. 4,6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ENPVVHFFKNIVTPRTP 17
DB      1 ENPVVHFFKNIVTPRTP 17

RESULT 6
US-09-813-463A-13
; Sequence 13, Application US/09813463A
; Patent No. US20020147303A1
; GENERAL INFORMATION:
; APPLICANT: WARREN, KENNETH G.
; APPLICANT: CATZ, INGRID
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC PROTEIN AND
; TITLE OF INVENTION: THE ADMINISTRATION OF MYELIN BASIC PROTEIN PEPTIDES TO
; TITLE OF INVENTION: MULTIPLE SCLEROSIS PATIENTS
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FILE REFERENCE: 098810/027 8740  
CURRENT APPLICATION NUMBER: US/09/813,463A  
CURRENT FILING DATE: 2002-01-11  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 13  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-813-463A-13

Query Match 92.6%; Score 87; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRT 16  
DB 2 ENPVVHFFKNIVTPRT 17

RESULT 7  
US-09-813-463A-13  
Sequence 13, Application US/09813463A  
Publication No. US20040072991A9  
GENERAL INFORMATION:  
APPLICANT: WARREN, KENNETH G.  
APPLICANT: CATZ, INGRID  
TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC PROTEIN AND  
TITLE OF INVENTION: THE ADMINISTRATION OF MYELIN BASIC PROTEIN PEPTIDES TO  
FILE REFERENCE: 098810/027 8740  
CURRENT APPLICATION NUMBER: US/09/813,463A  
CURRENT FILING DATE: 2002-01-11  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 13  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-813-463A-13

Query Match 92.6%; Score 87; DB 11; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRT 16  
DB 2 ENPVVHFFKNIVTPRT 17

RESULT 8  
US-09-909-460-37  
Sequence 37, Application US/09909460  
Publication No. US20020182258A1  
GENERAL INFORMATION:  
APPLICANT: Lunsford, Lynn B.  
APPLICANT: Putnam, David  
APPLICANT: Hedley, Mary Lynn  
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC  
FILE REFERENCE: 08191/014001  
CURRENT APPLICATION NUMBER: US/09/909,460  
CURRENT FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27  
NUMBER OF SEQ ID NOS: 114  
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 37  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-909-460-37

Query Match 87.2%; Score 82; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPR 15  
DB 1 ENPVVHFFKNIVTPR 15

RESULT 9  
US-09-847-172-41  
Sequence 41, Application US/09847172  
Publication No. US20030007978A1  
GENERAL INFORMATION:  
APPLICANT: OREGON HEALTH AND SCIENCES UNIVERSITY  
APPLICANT: BURREWS, GREGORY G.  
APPLICANT: VANDENBARK, ARTHUR A.  
TITLE OF INVENTION: RECOMBINANT MHC MOLECULES USEFUL FOR MANIPULATION OF ANTIGEN-SPECI  
FILE REFERENCE: 899-58137  
CURRENT APPLICATION NUMBER: US/09/847,172  
CURRENT FILING DATE: 2001-05-01  
PRIOR APPLICATION NUMBER: US 60/200,942  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: US 09/153,586  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: US 60/064,555  
PRIOR FILING DATE: 1997-10-10  
PRIOR APPLICATION NUMBER: US 60/064,552  
PRIOR FILING DATE: 1997-09-16  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 41  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificial peptide  
US-09-847-172-41

Query Match 87.2%; Score 82; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPR 15  
DB 1 ENPVVHFFKNIVTPR 15

RESULT 10  
US-09-872-836-37  
Sequence 37, Application US/09872836  
Publication No. US20040142475A1  
GENERAL INFORMATION:  
APPLICANT: Barman, Shikha P.  
APPLICANT: McKeever, Una  
APPLICANT: Hedley, Mary Lynne  
TITLE OF INVENTION: DELIVERY SYSTEMS FOR BIOACTIVE AGENTS  
FILE REFERENCE: 08191-018001  
CURRENT APPLICATION NUMBER: US/09/872,836  
CURRENT FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: US 60/208,830  
PRIOR FILING DATE: 2000-06-02  
NUMBER OF SEQ ID NOS: 120  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 37  
LENGTH: 15

TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-872-836-37

Query Match 87.2%; Score 82; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNITVPR 15  
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Db 1 ENPVVHFFKNITVPR 15  
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RESULT 11  
US-09-739-466C-5  
Sequence 5, Application US/09739466C  
Publication No. US20050107585A1  
GENERAL INFORMATION:  
APPLICANT: MURRAY, JOSEPH S  
APPLICANT: SIAMAN, TERUNA J  
APPLICANT: HU, YONGBO  
TITLE OF INVENTION: SIGNAL-1/SIGNAL-2 BIFUNCTIONAL PEPTIDE INHIBITORS  
FILE REFERENCE: 23902-08805  
CURRENT APPLICATION NUMBER: US/09/739,466C  
CURRENT FILING DATE: 2000-12-18  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: Patenlin Ver. 3.2  
SEQ ID NO 5  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-739-466C-5

Query Match 87.2%; Score 82; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNITVPR 15  
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Db 1 ENPVVHFFKNITVPR 15  
|||||

RESULT 12  
US-10-152-654-11  
Sequence 11, Application US/10152654  
Publication No. US20020137681A1  
GENERAL INFORMATION:  
APPLICANT: Steinman, Lawrence  
APPLICANT: Ruiz, Pedro  
TITLE OF INVENTION: Treatment of Demyelinating Autoimmune  
TITLE OF INVENTION: Disease with Ordered Peptides  
FILE REFERENCE: STAN-129  
CURRENT APPLICATION NUMBER: US/10/152,654  
CURRENT FILING DATE: 2002-05-20  
PRIOR APPLICATION NUMBER: US/09/606,254  
PRIOR FILING DATE: 2000-06-28  
PRIOR APPLICATION NUMBER: 60/142,479  
PRIOR FILING DATE: 1999-07-06  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Peptide  
US-10-152-654-11

Query Match 87.2%; Score 82; DB 13; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNITVPR 15

Db 1 ENPVVHFFKNITVPR 15  
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RESULT 13  
US-10-056-583-1  
Sequence 1, Application US/10056583  
Publication No. US20030064915A1  
GENERAL INFORMATION:  
APPLICANT: Presidents and Fellows of Harvard College  
APPLICANT: Strominger, Jack L.  
APPLICANT: Fridkis-Hareli, Masha  
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
FILE REFERENCE: 24655-017  
CURRENT APPLICATION NUMBER: US/10/056,583  
CURRENT FILING DATE: 2002-01-24  
PRIOR APPLICATION NUMBER: 60/263,569  
PRIOR FILING DATE: 2001-01-24  
NUMBER OF SEQ ID NOS: 99  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Immunodominant peptide of MBP, recognized by  
NAME/KEY: DOMAIN  
LOCATION: 85 - 99  
US-10-056-583-1

Query Match 87.2%; Score 82; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNITVPR 15  
|||||

Db 1 ENPVVHFFKNITVPR 15  
|||||

RESULT 14  
US-10-239-313A-142  
Sequence 142, Application US/10239313A  
Publication No. US20030175285A1  
GENERAL INFORMATION:  
APPLICANT: KLINGNER - HAMOUR, Christine  
APPLICANT: CORVAIA, Nathalie  
APPLICANT: BECK, Alain  
TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM  
FILE REFERENCE: 343 727 - US  
CURRENT APPLICATION NUMBER: US/10/239,313A  
CURRENT FILING DATE: 2002-09-19  
PRIOR APPLICATION NUMBER: FR 00/03711  
PRIOR FILING DATE: 2000-03-23  
PRIOR APPLICATION NUMBER: PCT 01/70772  
PRIOR FILING DATE: 2001-03-22  
NUMBER OF SEQ ID NOS: 697  
SOFTWARE: Patenlin Ver. 2.1  
SEQ ID NO 142  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-239-313A-142

Query Match 87.2%; Score 82; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNITVPR 15

Db 1 ENPVVHFFKNI VT PR 15

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RESULT 15
US-10-362-264-5
; Sequence 5, Application US/10362264
; Publication NO. US20030191063A1
; GENERAL INFORMATION:
; APPLICANT: Wraith, David
; APPLICANT: Anderton, Stephen
; APPLICANT: Mazza, Graziella
; APPLICANT: Ponsford, Mary
; APPLICANT: Streeter, Heather
; APPLICANT: The University of Bristol
; TITLE OF INVENTION: PEPTIDE SELECTION METHOD
; FILE REFERENCE: 1433.004US1
; CURRENT APPLICATION NUMBER: US/10/362,264
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/GB01/03702
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 0020618.5
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 0114547.3
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-362-264-5

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QY 1 ENPVVHFFKXIVTPR 15  
| | | | | | | | | |  
DB 1 ENPVVHFFKXIVTPR 15

Query Match 87.2%; Score 82; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: June 7, 2005, 09:50:47  
Job time : 144 secs

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Q-quant-24-X